

# Mesodinium chamaeleon data analysis, revision 3

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## Loading of packages and data

```
# LOAD RELEVANT PACKAGES
require(Rmisc) #has summarySE function, which is quite useful

## Loading required package: Rmisc
## Loading required package: lattice
## Loading required package: plyr
require(sciplot) #has bargraph.CI function

## Loading required package: sciplot
require(pracma)

## Loading required package: pracma

# IMPORT DATA
#setwd("~/GoogleSync/KarmaChamaeleon/JPhyc_R2/RAnalysis") # set working directory
dat<-read.csv('Meso_TS.csv',header=TRUE) # Timeseries of M. chamaeleon data
crypto.dat <- read.csv('Crypto_TS.csv',header=TRUE) # Timeseries of cryptophyte data
growth<-read.csv('GrowthRates.csv',header=TRUE) # Growthrates file
pe <- read.csv('MC_PEcureData.csv',header=TRUE) # M. chamaeleon photosynthesis-irradiance data
pe.crypto <- read.csv('Crypto_PEcuredata.csv',header=TRUE) # Cryptophyte photosynthesis-irradiance data
carbon <- read.csv('CHN.csv',header=TRUE) # CHN data

Cfix.mult <- 0.01728178 # The multiplier 0.01728178 converts from electrons per chlorophyll molecule per

# Adjust necessary data into numeric form; create ID columns
#str(dat)
dat$ID <- paste(dat$Prey,dat$Light,dat$Fed,dat$Rep,sep='.')
dat$Pmax_chl <- dat$Pmax*Cfix.mult # The multiplier converts from electrons per chlorophyll molecule per
dat$Pmax_cell <- dat$Pmax_chl*as.numeric(as.character(dat$corr_chl_p_cell))

## Warning: NAs introduced by coercion
dat$PI_chl <- dat$ETR_I*Cfix.mult
dat$PI_cell <- dat$PI_chl*as.numeric(as.character(dat$corr_chl_p_cell))

## Warning: NAs introduced by coercion
dat$chl_p_cell <- as.numeric(as.character(dat$corr_chl_p_cell)) # Sometimes R incorrectly imports data

## Warning: NAs introduced by coercion
dat$chl_p_mL <- dat$chl_p_cell*dat$MC_cellspmL/1000
dat$PlastidCount <- as.numeric(as.character(dat$PlastidCount))

## Warning: NAs introduced by coercion
```

```

#str(crypto.dat)
crypto.dat$ID <- paste(crypto.dat$Prey,crypto.dat$Light,crypto.dat$Rep,sep='.')
crypto.dat$Pmax_chl <- crypto.dat$Pmax*Cfix.mult
crypto.dat$Pmax_cell <- crypto.dat$Pmax_chl*crypto.dat$ChlpCell
crypto.dat$PI_chl <- crypto.dat$P_I*Cfix.mult
crypto.dat$PI_cell <- crypto.dat$PI_chl*crypto.dat$ChlpCell

pe$ETR.C <- pe$ETR*Cfix.mult # The multiplier converts from electrons per chlorophyll molecule per second

# SET PLOTTING PARAMETERS (COLOURS)
Acol <- 'red' # colour to plot rep A data
Bcol <- 'blue' # colour to plot rep B data
Ccol <- 'green' # colour to plot rep C data
Fedcol <- 'black'
Starvedcol <- 'gray80'
Cryptocol <- 'gray50'

SMcol <- 'firebrick'
RScol <- 'lightcoral'
CMcol <- 'seagreen'
HPcol <- 'turquoise3'
preycolvec <- c(CMcol,HPcol,RScol,SMcol)

days <- unique(dat$ExptDay)

```

## Computations

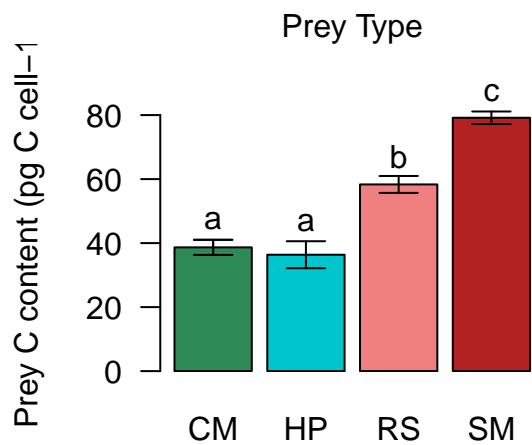
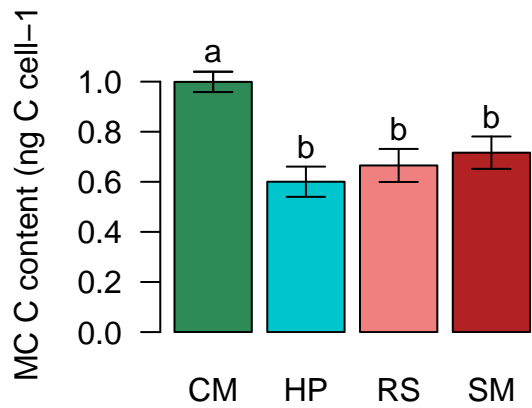
### Revision 1: Supplemental Figure: C per cell

```

par(mar=c(4,4,1,1),mfrow=c(2,1))
bargraph.CI(Prey,ngC_cell,data=carbon[carbon$Species=='MC',],las=1,xlab='Prey Type',ylab='MC C content')
# TukeyHSD(aov(ngC_cell~Prey,data=carbon[carbon$Species=='MC',]))

bargraph.CI(Species,ngC_cell*1000,data=carbon[carbon$Species!='MC',],las=1,xlab='Cryptophyte',ylab='Prey')

```



### Cryptophyte

```
#TukeyHSD(aov(ngC_cell~Species,data=carbon[carbon$Species!='MC',]))
```

### Revision 1: Incorporating C per cell

```
# M. chamaeleon
MC.C <- summarySE(data=carbon[carbon$Species=='MC',],measurevar='ngC_cell',groupvar='Prey')
dat$Cpercell <- MC.C$ngC_cell[match(dat$Prey,MC.C$Prey)]
dat$ChlperC <- dat$chl_p_cell/dat$Cpercell
dat$Pmax_C <- dat$Pmax_cell/dat$Cpercell
dat$PI_C <- dat$PI_cell/dat$Cpercell

# Cryptophytes
prey.C <- summarySE(data=carbon[carbon$Species!='MC',],measurevar='ngC_cell',groupvar='Species')
crypto.dat$Cpercell <- prey.C$ngC_cell[match(crypto.dat$Prey,prey.C$Species)]
crypto.dat$ChlperC <- crypto.dat$ChlpCell/crypto.dat$Cpercell
crypto.dat$Pmax_C <- crypto.dat$Pmax_cell/crypto.dat$Cpercell
crypto.dat$PI_C <- crypto.dat$PI_cell/crypto.dat$Cpercell
```

## Computing maxima

```
# Pick max crypto response
```

```
crypto.max <- as.data.frame(unique(crypto.dat$ID))
colnames(crypto.max) <- c('ID')
crypto.max$Prey <- crypto.dat$Prey[match(crypto.max$ID,crypto.dat$ID)]
crypto.max$Light <- crypto.dat$Light[match(crypto.max$ID,crypto.dat$ID)]
crypto.max$Rep <- crypto.dat$Rep[match(crypto.max$ID,crypto.dat$ID)]
crypto.max$chl <- NaN; crypto.max$FvFm <- NaN; crypto.max$P_I <- NaN; crypto.max$a <- NaN; crypto.max$Pmax <- NaN; crypto.max$PI_C <- NaN; crypto.max$Pmax_C <- NaN; crypto.max$ChlperC <- NaN
```

```
# Revision 1:
crypto.max$PI_C <- NaN; crypto.max$Pmax_C <- NaN; crypto.max$ChlperC <- NaN

for(i in 1:length(unique(crypto.dat$ID))){
  hold <- crypto.dat[crypto.dat$ID==unique(crypto.dat$ID)[i],]
  crypto.max$chl[i] <- max(hold$ChlpCell,na.rm=TRUE)
  hold2 <- hold
  if(hold$Prey[1]=='CM'){ hold2 <- hold[hold$ExptDay%in%c(0,1),]}
  crypto.max$FvFm[i] <- max(hold2$Fv.Fm,na.rm=TRUE)
  hold <- hold[hold$ExptDay%in%c(0,1,2,4),]
  crypto.max$P_I[i] <- max(hold$P_I,na.rm=TRUE)
  crypto.max$Pmax[i] <- max(hold$Pmax,na.rm=TRUE)
  crypto.max$a[i] <- max(hold$a,na.rm=TRUE)
  crypto.max$Pmax_chl[i] <- max(hold$Pmax_chl,na.rm=TRUE)
  crypto.max$Pmax_cell[i] <- max(hold$Pmax_cell,na.rm=TRUE)
  crypto.max$PI_chl[i] <- max(hold$PI_chl,na.rm=TRUE)
  crypto.max$PI_cell[i] <- max(hold$PI_cell,na.rm=TRUE)
  # Revision 1:
  crypto.max$PI_C[i] <- max(hold$PI_C,na.rm=TRUE)
  crypto.max$Pmax_C[i] <- max(hold$Pmax_C,na.rm=TRUE)
  crypto.max$ChlperC[i] <- max(hold$ChlperC,na.rm=TRUE)
}
```

```
MC.max <- as.data.frame(unique(dat$ID))
colnames(MC.max) <- c('ID')
MC.max$Prey <- dat$Prey[match(MC.max$ID,dat$ID)]
MC.max$Light <- dat$Light[match(MC.max$ID,dat$ID)]
MC.max$Fed <- dat$Fed[match(MC.max$ID,dat$ID)]
MC.max$Rep <- dat$Rep[match(MC.max$ID,dat$ID)]
MC.max$chl <- NaN; MC.max$FvFm <- NaN; MC.max$P_I <- NaN; MC.max$a <- NaN; MC.max$Pmax <- NaN; MC.max$PI_C <- NaN; MC.max$Pmax_C <- NaN; MC.max$ChlperC <- NaN
```

```
# Revision 1:
```

```
MC.max$ChlperC <- NaN; MC.max$Pmax_C <- NaN; MC.max$PI_C <- NaN
```

```
for(i in 1:length(unique(dat$ID))){
  hold <- dat[dat$ID==unique(dat$ID)[i],]
  hold <- hold[hold$ExptDay%in%c(0,1,2,4,6),]
  MC.max$P_I[i] <- max(hold$ETR_I,na.rm=TRUE)
  MC.max$a[i] <- max(hold$a,na.rm=TRUE)
  MC.max$Pmax[i] <- max(hold$Pmax,na.rm=TRUE)
  MC.max$Pmax_chl[i] <- max(hold$Pmax_chl,na.rm=TRUE)
  MC.max$Pmax_cell[i] <- max(hold$Pmax_cell,na.rm=TRUE)
}
```

```

MC.max$PI_chl[i] <- max(hold$PI_chl,na.rm=TRUE)
MC.max$PI_cell[i] <- max(hold$PI_cell,na.rm=TRUE)
hold <- hold[hold$ExptDay%in%c(0,1,2,4),]
MC.max$chl[i] <- max(hold$chl_p_cell,na.rm=TRUE)
MC.max$FvFm[i] <- max(hold$FvFm,na.rm=TRUE)
MC.max$plastids[i] <- max(hold$PlastidCount,na.rm=TRUE)

# Revision 1:
MC.max$ChlperC[i] <- max(hold$ChlperC,na.rm=TRUE)
MC.max$Pmax_C[i] <- max(hold$Pmax_C,na.rm=TRUE)
MC.max$PI_C[i] <- max(hold$PI_C,na.rm=TRUE)
}

crypto.max$Prey.Light <- paste(crypto.max$Prey,crypto.max$Light,sep='.')
MC.max$Prey.Light <- paste(MC.max$Prey,MC.max$Light,sep='.')
MC.max$Treat.Rep <- paste('1802',MC.max$ID,sep='.')

MC.max$relFvFm <- NaN
MC.max$relP_I <- NaN
MC.max$rela <- NaN
MC.max$relPmax <- NaN
MC.max$relPmax_chl <- NaN
MC.max$relPI_chl <- NaN

# Revision 1:
MC.max$relPI_C <- NaN
MC.max$relPmax_C <- NaN

for(i in 1:dim(MC.max)[1]){
  # Compute relative MC FvFm
  callID <- MC.max$Prey.Light[i]
  MC.max$relFvFm[i] <- MC.max$FvFm[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$FvFm,na.rm=TRUE)

  # Compute relative MC P_I
  MC.max$relP_I[i] <- MC.max$P_I[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$P_I,na.rm=TRUE)

  # Compute relative MC a
  MC.max$rela[i] <- MC.max$a[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$a,na.rm=TRUE)

  # Compute relative MC P_max
  MC.max$relPmax[i] <- MC.max$Pmax[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$Pmax,na.rm=TRUE)

  # Compute relative MC P_max per chl
  MC.max$relPmax_chl[i] <- MC.max$Pmax_chl[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$Pmax_chl,na.rm=TRUE)

  # Compute relative MC P_I per chl
  MC.max$relPI_chl[i] <- MC.max$PI_chl[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$PI_chl,na.rm=TRUE)

  # Revision 1:
  # Compute relative MC P_I per C
  MC.max$relPI_C[i] <- MC.max$PI_C[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$PI_C,na.rm=TRUE)
  # Compute relative MC P_max per C

```

```

MC.max$relPmax_C[i] <- MC.max$Pmax_C[i]/mean(crypto.max[crypto.max$Prey.Light==callID,]$Pmax_C,na.rm=TRUE)
}

dat$Treat.Rep <- paste(dat$MCstrain,dat$Prey,dat$Light,dat$Fed,dat$Rep,sep='.')
#treat.data <- as.data.frame(unique(dat$Treatment))
growth$Treat.Rep <- paste(growth$MCstrain,growth$Prey,growth$Light,growth$Fed,growth$Rep,sep='.')

growth$ic <- NaN
growth$preyic <- NaN
growth$max <- NaN
growth$relincrease <- NaN
growth$relincreaseperprey <- NaN
for(i in 1:dim(growth)[1]){
  dat.hold <- dat[dat$Treat.Rep==growth$Treat.Rep[i],]
  growth$ic[i] <- dat.hold[dat.hold$ExptDay==0,]$MC_cellspmL
  growth$preyic[i] <- dat.hold[dat.hold$ExptDay==0,]$Prey_cellspmL
  growth$max[i] <- max(dat.hold$MC_cellspmL,na.rm=TRUE)
  growth$relincrease[i] <- growth$max[i]/growth$ic[i]
  growth$relincreaseperprey[i] <- (growth$max[i]-growth$ic[i])/growth$preyic[i]
}

growth$deltarelincreasefed <- NaN
for(i in 1:dim(growth[growth$Fed=='Y',])[1]){
  growth[growth$Fed=='Y',]$deltarelincreasefed[i] <- growth[growth$Fed=='Y',]$relincrease[i]-growth[growth$Fed=='Y',]$ic[i]
}

growth$TotPreyCons <- rep(0,dim(growth)[1])
times <- c(0,1,2,4,6,8,10,12,14)

for(i in 1:length(unique(dat$Treat.Rep))){
  callID <- unique(dat$Treat.Rep)[i] # Select the dataset of interest
  if(growth[growth$Treat.Rep==callID,]$Fed=='Y'){ # If this is a fed dataset
    hold <- dat[dat$Treat.Rep==callID,]
    hold <- hold[!is.na(hold$MC_cellspmL),]
    prey <- hold$Prey_cellspmL
    MC <- hold$MC_cellspmL
    MC_init <- MC[1]
    graz <- growth[growth$Treat.Rep==callID,]$g
    fcn <- graz*prey
    for(j in 1:length(hold)[1]){if(is.nan(fcn[j])){fcn[j]<-0}}
    growth[growth$Treat.Rep==callID,]$TotPreyCons <- trapz(hold$ExptDay,fcn)
    growth[growth$Treat.Rep==callID,]$MC_init <- MC_init
  }
}

growth$PreyperMC <- growth$TotPreyCons/growth$ic

```

```

# photosynthesis contributions

growth$chl.loss.rate <- NaN
growth$plastid.loss.rate <- NaN
growth$FvFm.decline <- NaN
growth$chl.decline <- NaN
growth$FvFm.pctdecline <- NaN
growth$chl.pctdecline <- NaN
growth$PI.perchl <- NaN
growth$Cfixforchl <- NaN
growth$chl.res.time <- NaN
growth$C.perchl <- NaN
growth$C.perprey <- NaN
growth$C.fromprey <- NaN
growth$C.fixed <- NaN
growth$C.fixed2 <- NaN

# Revision 1:
growth$Pmax.change <- NaN
growth$a.change <- NaN
growth$Pmax.pctchange <- NaN
growth$a.pctchange <- NaN

IDs <- unique(growth$Treat.Rep)
times <- c(0,1,2,4,6,8,10,12,14)
tsteps <- 5 # number of timesteps to use

for(i in 1:length(IDs)){
  # Choose the dataset
  callID <- IDs[i]
  hold <- dat[dat$Treat.Rep==callID,]

  # Determine rate of chlorophyll loss over first week
  chls <- log(hold$chl_p_cell)
  lm1 <- lm(chls[1:tsteps]~times[1:tsteps])
  if(hold$Prey[1]=="CM"){ lm1 <- lm(chls[2:tsteps]~times[2:tsteps]) }
  if(hold$Light[1]==10&hold$Rep[1]=='B'){ lm1 <- lm(chls[1:4]~times[1:4]) }

  growth[growth$Treat.Rep==callID,]$chl.loss.rate <- summary(lm1)$coefficients[2,1]

  # Determine rate of plastid loss over first 48 hrs
  plastids <- log(hold$PlastidCount)
  lm2 <- lm(plastids[1:3]~times[1:3])
  growth[growth$Treat.Rep==callID,]$plastid.loss.rate <- summary(lm2)$coefficients[2,1]

  # Determine overall decline in Fv/Fm
  FvFm.init <- hold$FvFm[1]
  FvFm.min <- min(hold$FvFm,na.rm=TRUE)
  growth[growth$Treat.Rep==callID,]$FvFm.decline <- FvFm.init-FvFm.min
  growth[growth$Treat.Rep==callID,]$FvFm.pctdecline <- (FvFm.init-FvFm.min)/FvFm.init

  # Determine overall change in alpha
  a.init <- hold$a[1]

```

```

a.end <- hold$a[dim(hold)[1]]
if(hold$Prey[1]=="CM"){if(hold$Light[1]==100){a.end <- hold$a[dim(hold)[1]-1]}} # Using Day 12 data
growth[growth$Treat.Rep==callID,]$a.change <- a.init-a.end
growth[growth$Treat.Rep==callID,]$a.pctchange <- (a.init-a.end)/a.init

# Determine overall change in Pmax
p.init <- hold$Pmax[1]
p.end <- hold$Pmax[dim(hold)[1]]
if(hold$Prey[1]=="CM"){if(hold$Light[1]==100){p.end <- hold$Pmax[dim(hold)[1]-1]}} # Using Day 12 data
growth[growth$Treat.Rep==callID,]$Pmax.change <- p.init-p.end
growth[growth$Treat.Rep==callID,]$Pmax.pctchange <- (p.init-p.end)/p.init

# Determine overall decline in chl-a
chla.init <- hold$chl_p_cell[1]
chla.min <- min(hold$chl_p_cell,na.rm=TRUE)
growth[growth$Treat.Rep==callID,]$chl.decline <- chla.init-chla.min
growth[growth$Treat.Rep==callID,]$chl.pctdecline <- (chla.init-chla.min)/chla.init

# Chlorophyll residence time
growth[growth$Treat.Rep==callID,]$chl.res.time = -1/(growth[growth$Treat.Rep==callID,]$chl.loss.rate)

# Carbon fixed during that residence time
PIs <- hold$PI_chl
PI.mean <- mean(PIs[1:tsteps],na.rm=TRUE)
growth[growth$Treat.Rep==callID,]$PI.perchl <- PI.mean
growth[growth$Treat.Rep==callID,]$C.perchl <- PI.mean*growth[growth$Treat.Rep==callID,]$chl.res.time

# Carbon fixed per prey cell
preychl <- mean(crypto.max[crypto.max$Prey==hold$Prey[1]&crypto.max$Light==hold$Light[1],]$chl,na.rm=TRUE)
growth[growth$Treat.Rep==callID,]$C.perprey <- preychl*growth[growth$Treat.Rep==callID,]$C.perchl

# Carbon fixed from all prey across the experiment
preycons <- mean(growth[growth$Fed=='Y'&growth$Prey==hold$Prey[1]&growth$Light==hold$Light[1],]$Prey)
growth[growth$Treat.Rep==callID,]$C.fromprey <- preycons*growth[growth$Treat.Rep==callID,]$C.perprey

# Carbon fixed, calculated as integral of chl-a/cell * PI_chl
hold <- hold[!is.na(hold$PI_cell),]
growth[growth$Treat.Rep==callID,]$C.fixed <- trapz(hold$ExptDay,hold$chl_p_cell*hold$PI_chl*12) # m

# Carbon fixed, calculated as integral of chl-a/mL * PI_chl divided by initial cells
hold <- hold[!is.na(hold$chl_p_mL),]
growth[growth$Treat.Rep==callID,]$C.fixed2 <- trapz(hold$ExptDay,hold$PI_chl*12*hold$chl_p_mL)/hold$chl_p_mL

}

growth$deltaCfixed <- NaN
for(i in 1:dim(growth[growth$Fed=='Y',])[1]){
  growth[growth$Fed=='Y',]$deltaCfixed[i] <- growth[growth$Fed=='Y',]$C.fixed2[i]-growth[growth$Fed=='N',]$C.fixed2[i]
}

```



## Visualizing Data

Figure 1: Loss of photosynthetic capacity in starved cultures

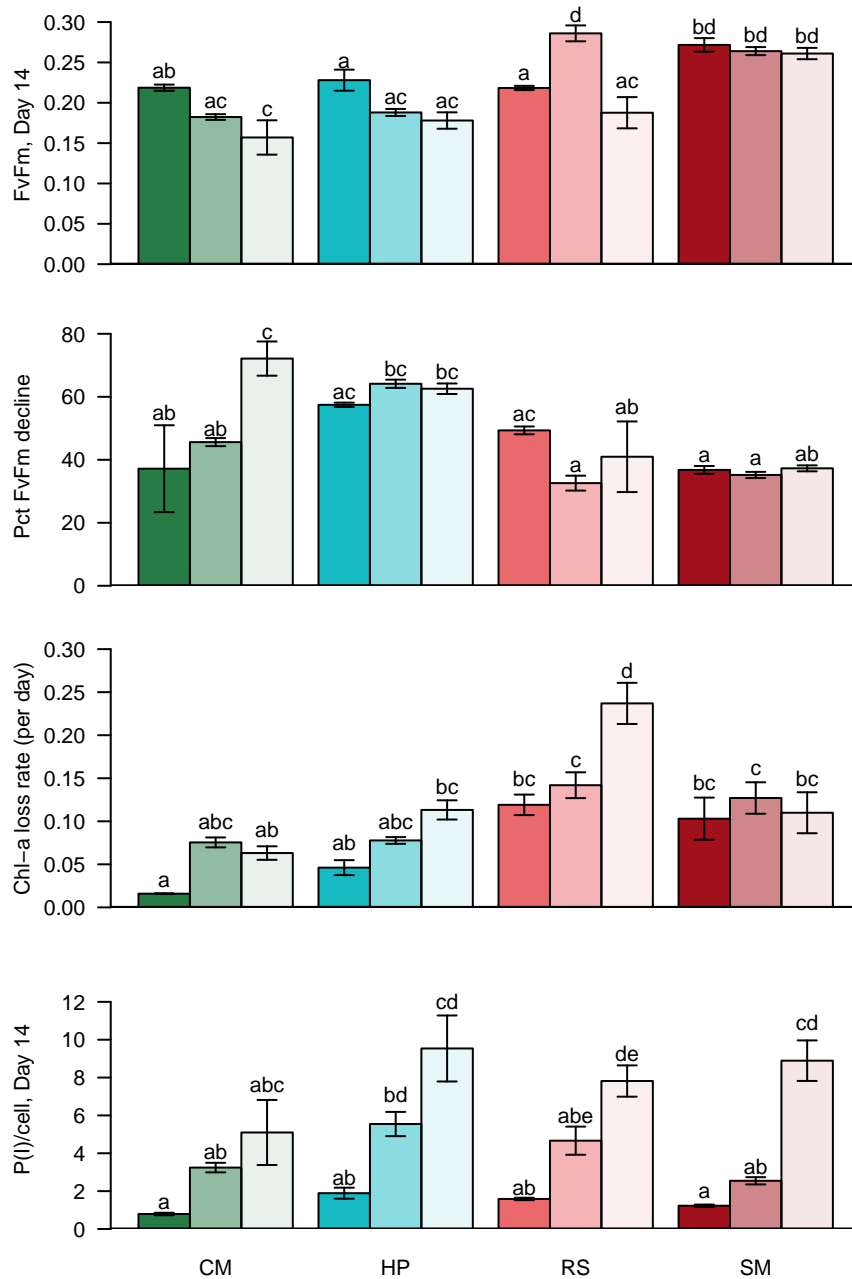
```
par(mar=c(2,4,0.5,0.5),mfrow=c(4,1))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

# FvFm at day 14
bargraph.CI(Prey,FvFm,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.05,la
#TukeyHSD(aov(FvFm~Prey*as.factor(Light),data=dat[dat$Fed=='N'&dat$ExptDay==14,]))

# decline in FvFm
#bargraph.CI(Prey,FvFm.decline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,la
bargraph.CI(Prey,100*FvFm.pctdecline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0
#TukeyHSD(aov(FvFm.pctdecline~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))

# pigment decay rate
bargraph.CI(Prey,-1*(chl.loss.rate),group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.0
#TukeyHSD(aov(-1*(chl.loss.rate)~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))

# P(I) at day 14
bargraph.CI(Prey,PI_cell,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.0
```



```
#TukeyHSD(aov(PI_cell~Prey*as.factor(Light),data=dat[dat$Fed=='N'&dat$ExptDay==14,]))
```

# Even after 14 days of starvation, *M. chamaeleon* acclimated to all four types showed sustained photosynthesis

Figure 1, revision 1: Loss of photosynthetic capacity in starved cultures

```
par(mar=c(2,4,0.3,0.5),mfrow=c(3,2))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

# FvFm at day 14
bargraph.CI(Prey,FvFm,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.05,1)
#TukeyHSD(aov(FvFm~Prey*as.factor(Light),data=dat[dat$Fed=='N'&dat$ExptDay==14,]))
```

```

# P(I) at day 14
bargraph.CI(Prey,PI_ch1,group=Light,data=dat[dat$Fed=='N'&dat$ExptDay==14,],legend=FALSE,err.width=0.05)
#TukeyHSD(aov(PI_ch1~as.factor(Light)*Prey,data=dat[dat$Fed=='N'&dat$ExptDay==14,]))

# decline in FvFm
#bargraph.CI(Prey,FvFm.decline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=3)
bargraph.CI(Prey,100*FvFm.pctdecline,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05)
#TukeyHSD(aov(FvFm.pctdecline~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))

# pigment decay rate
bargraph.CI(Prey,-1*(chl.loss.rate),group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=3)
#TukeyHSD(aov(-1*(chl.loss.rate)~Prey*as.factor(Light),data=growth[growth$Fed=='N',]))

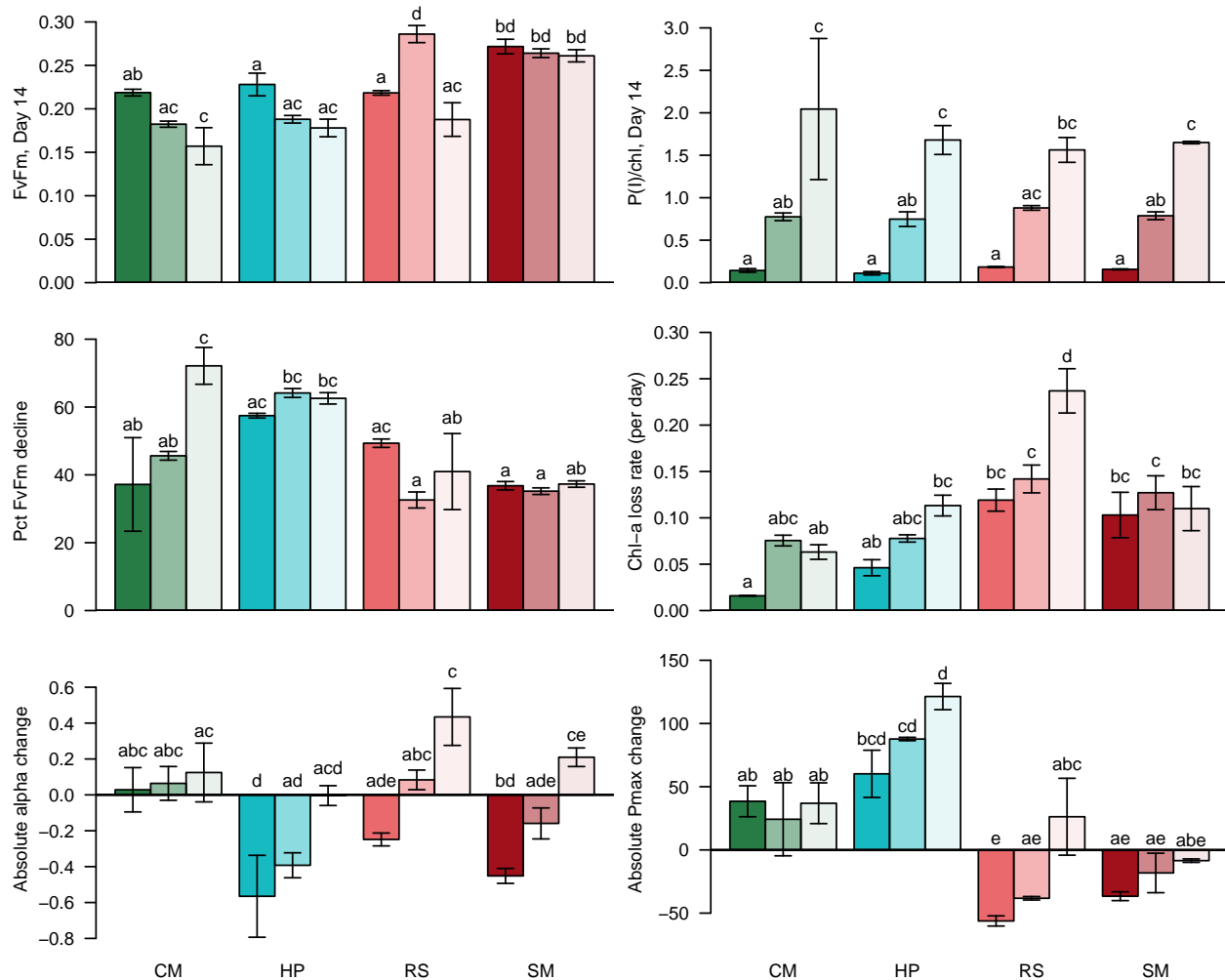
# Revision 1:
# pct change in alpha
# bargraph.CI(Prey,-100*a.pctchange,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=3)

# pct change in Pmax
# bargraph.CI(Prey,-100*Pmax.pctchange,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=3)

# change in alpha
bargraph.CI(Prey,-a.change,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=3)
#TukeyHSD(aov(a.change~as.factor(Light)*Prey,data=growth[growth$Fed=='N',]))

# change in Pmax
bargraph.CI(Prey,-Pmax.change,group=Light,data=growth[growth$Fed=='N',],legend=FALSE,err.width=0.05,las=3)

```



```
#TukeyHSD(aov(Pmax.change~as.factor(Light)*Prey,data=growth[growth$Fed=='N',]))
```

Supplementary Figure: PE curves over time, by prey and light level, measured in electron transport per chlorophyll-a

```
# Note: this is in electron transport rate (electrons per s per chl-a)

pe.summ <- summarySE(data=pe, 'ETR', groupvars=c('Prey', 'Light', 'Fed', 'ExptDay', 'PAR'), na.rm=TRUE)

preychoice_set <- c('CM', 'HP', 'RS', 'SM')
lightchoice_set <- c(10, 50, 100)
ymax_set <- c(100, 130, 200)

days <- unique(pe.summ$ExptDay)
bgvec <- rev(c('gray90', 'gray80', 'gray70', 'gray60', 'gray50', 'gray40', 'gray30', 'gray20', 'black'))

par(mar=c(1, 1, 0.5, 0.5))
```

```

layout(matrix(c(rep(c(13,1,1,1,2,2,2,3,3,3,4,4,4),3),rep(c(13,5,5,5,6,6,6,7,7,7,8,8,8),3),rep(c(13,9,9,9,10,10,10,11,11,11,12,12,12),3)),3),rep(c(13,9,9,9,10,10,10,11,11,11,12,12,12),3),rep(c(13,9,9,9,10,10,10,11,11,11,12,12,12),3))

## Warning in matrix(c(rep(c(13, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4), 3),
## rep(c(13, : data length [133] is not a sub-multiple or multiple of the
## number of rows [10])
for(lightctr in 1:length(lightchoice_set)){
  lightchoice <- lightchoice_set[lightctr]
  ymaxchoice <- ymax_set[lightctr]

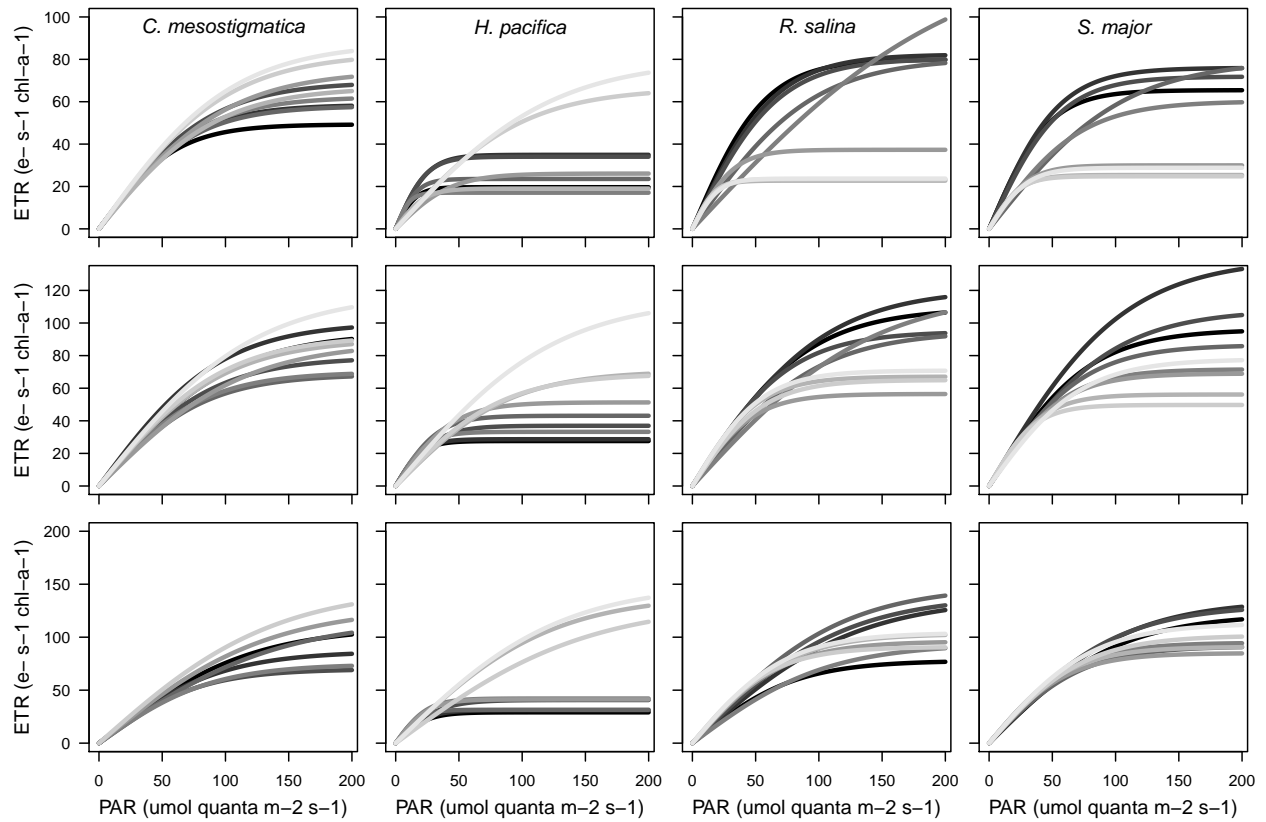
for(preycctr in 1:length(preychoice_set)){
  preychoice = preychoice_set[preycctr]

hold <- pe.summ[pe.summ$Prey==preychoice&pe.summ$Light==lightchoice&pe.summ$Fed=='N',]

plot(hold$PAR,hold$ETR,bg=bgvec[as.factor(hold$ExptDay)],pch=21,cex=1.5,xlab='',ylab='',las=1,ylim=c(0,
Iset <- seq(from = 0, to = 200,length.out=1000)
for(i in 1:length(days)){
  Pmax <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$Pmax)
  alpha <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$a)
  # Curves were fit with the Jassby & Platt hyperbolic tangent function:
  # ETR = P * tanh(a * PAR / P)

  ETRset <- Pmax*tanh(alpha*Iset/Pmax)
  lines(Iset,ETRset,col=bgvec[i],lwd=3)
}
if(lightctr==3){mtext('PAR (umol quanta m-2 s-1)',side=1,line=2.5,cex=0.8)}
if(preycctr==1){mtext('ETR (e- s-1 chl-a-1)',side=2,line=3,cex=0.8)}
if(lightctr==1){
  if(preycctr==1){mtext(substitute(paste(italic('C. mesostigmatica'))),side=3,line=-1.75,cex=.8)}
  if(preycctr==2){mtext(substitute(paste(italic('H. pacifica'))),side=3,line=-1.75,cex=.8)}
  if(preycctr==3){mtext(substitute(paste(italic('R. salina'))),side=3,line=-1.5,cex=.8)}
  if(preycctr==4){mtext(substitute(paste(italic('S. major'))),side=3,line=-1.75,cex=.8)}
}
}}

```



Supplementary Figure: PE curves over time, by prey and light level, measured in carbon fixation per cell

```

dat$Treat.Rep.Day <- paste(dat$Treat.Rep,dat$ExptDay,sep='.')
pe$Treat.Rep.Day <- paste(pe$MCstrain,pe$Prey,pe$Light,pe$Fed,pe$Rep,pe$ExptDay,sep='.')
pe$chl <- dat$corr_chl_p_cell[match(pe$Treat.Rep.Day,dat$Treat.Rep.Day)]
pe$ETR.cell <- pe$ETR.C*as.numeric(as.character(pe$chl))

## Warning: NAs introduced by coercion
pe.summ <- summarySE(data=pe,'ETR.cell',groupvars=c('Prey','Light','Fed','ExptDay','PAR'),na.rm=TRUE)

preychoice_set <- c('CM','HP','RS','SM')
lightchoice_set <- c(10,50,100)
ymax_set <- c(160,160,160)*12.01/44.01

days <- unique(pe.summ$ExptDay)
bgvec <- rev(c('gray90','gray80','gray70','gray60','gray50','gray40','gray30','gray20','black'))

par(mar=c(1,1,0.5,0.5))
layout(matrix(c(rep(c(13,1,1,1,2,2,2,3,3,3,4,4,4),3),rep(c(13,5,5,5,6,6,6,7,7,7,8,8,8),3),rep(c(13,9,9,9,10,10,10,11,11,11,12,12,12),3)),3,1))

## Warning in matrix(c(rep(c(13, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4), 3),
## rep(c(13, : data length [133] is not a sub-multiple or multiple of the
## number of rows [10]

```

```

for(lightctr in 1:length(lightchoice_set)){
  lightchoice <- lightchoice_set[lightctr]
  ymaxchoice <- ymax_set[lightctr]

for(preycctr in 1:length(preychoice_set)){
  preychoice = preychoice_set[preycctr]

hold <- pe.summ[pe.summ$Prey==preychoice&pe.summ$Light==lightchoice&pe.summ$Fed=='N',]

plot(hold$PAR,hold$ETR.cell,bg=bgvec[as.factor(hold$ExptDay)],pch=21,cex=1.5,xlab='',ylab='',las=1,ylim=
Iset <- seq(from = 0, to = 200,length.out=1000)
for(i in 1:length(days)){
  Pmax <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$Pmax)
  alpha <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$a)*
  # Curves were fit with the Jassby & Platt hyperbolic tangent function:
  # ETR = P * tanh(a * PAR / P)

  ETRset <- Pmax*tanh(alpha*Iset/Pmax)
  lines(Iset,ETRset,col=bgvec[i],lwd=3)
}
if(lightctr==3){mtext('PAR (umol quanta m-2 s-1)',side=1,line=2.5,cex=0.8)}
if(preycctr==1){mtext('C fix (pg C cell-1 hr-1)',side=2,line=3,cex=0.8)}
if(lightctr==1){
  if(preycctr==1){mtext(substitute(paste(italic('C. mesostigmatica'))),side=3,line=-1.75,cex=.8)}
  if(preycctr==2){mtext(substitute(paste(italic('H. pacifica'))),side=3,line=-1.75,cex=.8)}
  if(preycctr==3){mtext(substitute(paste(italic('R. salina'))),side=3,line=-1.75,cex=.8)}
  if(preycctr==4){mtext(substitute(paste(italic('S. major'))),side=3,line=-1.75,cex=.8)}
}
}}

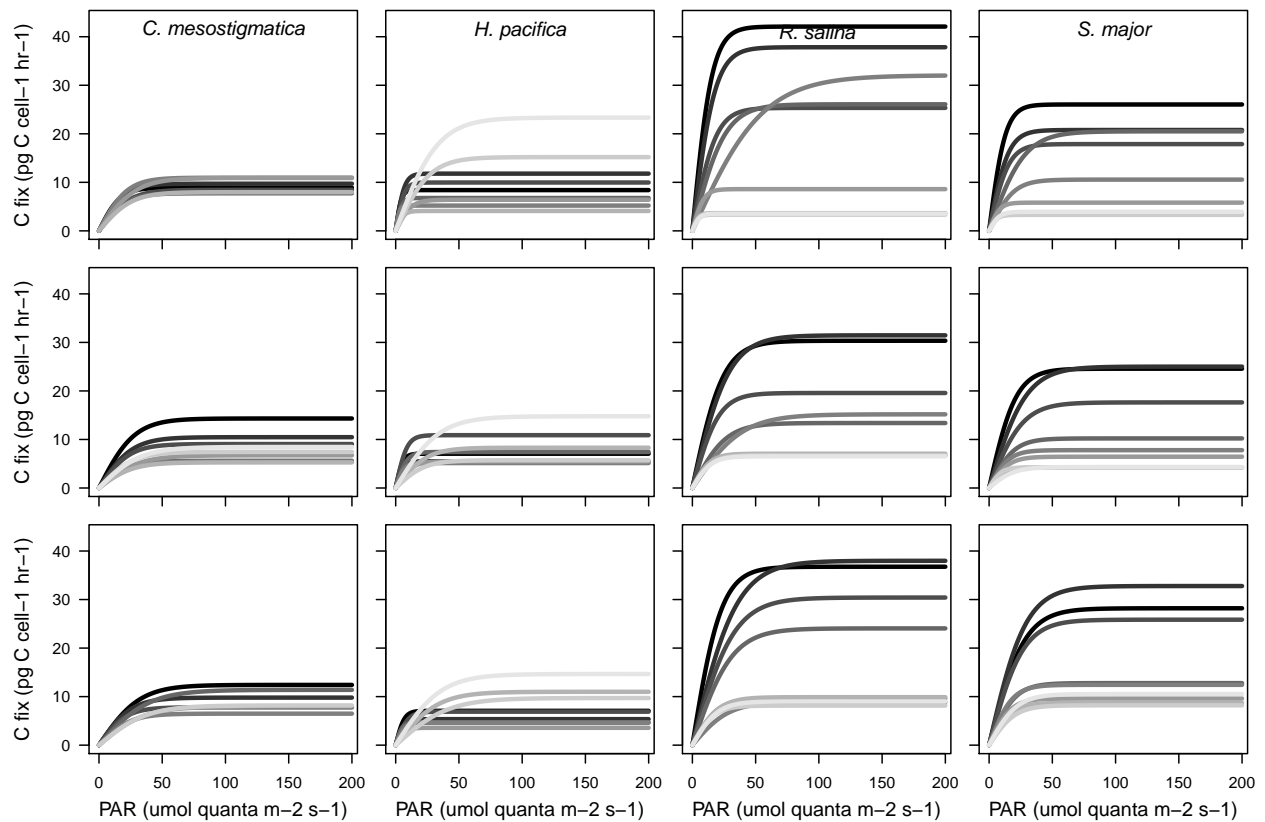
```

```

## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion

## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion

```



Supplementary Figure, Revision: PE curves over time, by prey and light level, measured in carbon fixation per C

```

dat$Treat.Rep.Day <- paste(dat$Treat.Rep, dat$ExptDay, sep='.')
pe$Treat.Rep.Day <- paste(pe$MCstrain, pe$Prey, pe$Light, pe$Fed, pe$Rep, pe$ExptDay, sep='.')
pe$chl <- dat$corr_chl_p_cell[match(pe$Treat.Rep.Day, dat$Treat.Rep.Day)]
pe$ETR.cell <- pe$ETR.C * as.numeric(as.character(pe$chl))

## Warning: NAs introduced by coercion
pe.summ <- summarySE(data=pe, 'ETR.cell', groupvars=c('Prey', 'Light', 'Fed', 'ExptDay', 'PAR'), na.rm=TRUE)

preychoice_set <- c('CM', 'HP', 'RS', 'SM')
lightchoice_set <- c(10, 50, 100)
ymax_set <- c(250, 250, 250) * 12.01 / 44.01

days <- unique(pe.summ$ExptDay)
bgvec <- rev(c('gray90', 'gray80', 'gray70', 'gray60', 'gray50', 'gray40', 'gray30', 'gray20', 'black'))

par(mar=c(1, 1, 0.5, 0.5))
layout(matrix(c(rep(c(13, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4), 3), rep(c(13, 5, 5, 5, 6, 6, 6, 7, 7, 7, 8, 8, 8), 3), rep(c(13, 9, 9, 9, 10, 10, 10, 11, 11, 11, 12, 12, 12), 3)), 2, 1))

## Warning in matrix(c(rep(c(13, 1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4), 3),
## rep(c(13, : data length [133] is not a sub-multiple or multiple of the
## number of rows [10]

```



```

for(lightctr in 1:length(lightchoice_set)){
  lightchoice <- lightchoice_set[lightctr]
  ymaxchoice <- ymax_set[lightctr]

for(preycctr in 1:length(preychoice_set)){
  preychoice = preychoice_set[preycctr]
  preyC <- mean(carbon[carbon$Prey==preychoice_set[preycctr],]$ngC_cell)

hold <- pe.summ[pe.summ$Prey==preychoice&pe.summ$Light==lightchoice&pe.summ$Fed=='N',]

plot(hold$PAR,hold$ETR.cell/preyC,bg=bgvec[as.factor(hold$ExptDay)],pch=21,cex=1.5,xlab='',ylab='',las=1)
if(lightctr==3){axis(side=1,labels=T)}else{axis(side=1,labels=F)}; if(preycctr==1){axis(side=2,labels=T),las=1}
Iset <- seq(from = 0, to = 200,length.out=1000)
for(i in 1:length(days)){
  Pmax <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$Pmax)
  alpha <- mean(dat[dat$Prey==preychoice&dat$Light==lightchoice&dat$Fed=='N'&dat$ExptDay==days[i],]$a)*
  # Curves were fit with the Jassby & Platt hyperbolic tangent function:
  # ETR = P * tanh(a * PAR / P)

  ETRset <- Pmax*tanh(alpha*Iset/Pmax)
  lines(Iset,ETRset,col=bgvec[i],lwd=3)
}
if(lightctr==3){mtext('PAR (umol quanta m-2 s-1)',side=1,line=2.5,cex=0.8)}
if(preycctr==1){mtext('C fix (pg C cell-1 hr-1)',side=2,line=3,cex=0.8)}
if(lightctr==1){
  if(preycctr==1){mtext(substitute(paste(italic('C. mesostigmatica'))),side=3,line=-1.75,cex=.8)}
  if(preycctr==2){mtext(substitute(paste(italic('H. pacifica'))),side=3,line=-1.75,cex=.8)}
  if(preycctr==3){mtext(substitute(paste(italic('R. salina'))),side=3,line=-1.5,cex=.8)}
  if(preycctr==4){mtext(substitute(paste(italic('S. major'))),side=3,line=-1.75,cex=.8)}
}
}}

## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion

## Warning in mean(as.numeric(as.character(dat[dat$Prey == preychoice & dat
## $Light == : NAs introduced by coercion

```

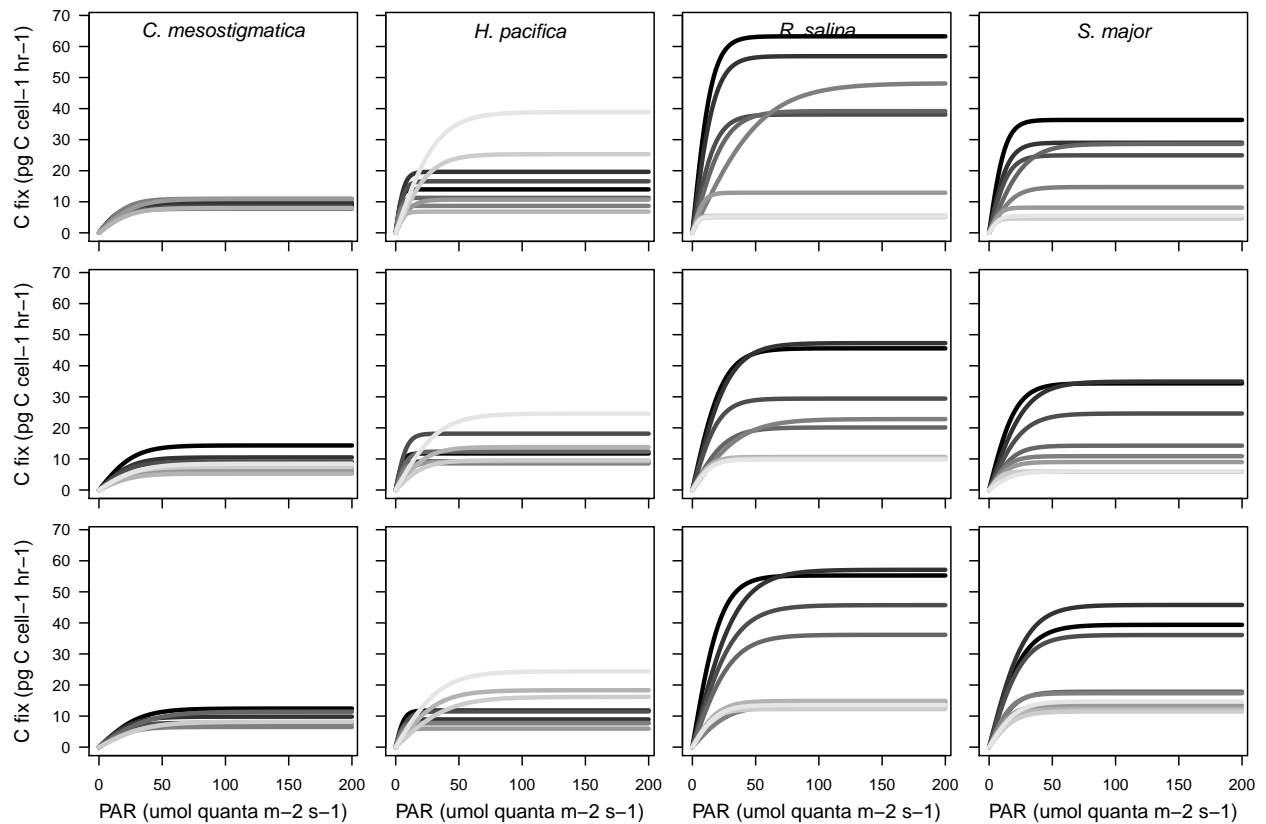


Figure 2: Maximum photosynthetic performance

```
#quartz(height=6.65,width=4)
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
layout(matrix(c(1,1,2,2,3,3,4,4,5)))
par(mar=c(.5,4,0.5,2))

# Panel A: Fv/Fm
bargraph.CI(Prey,FvFm,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y'],,ylim=c(0.35,0.6),las=1,space=0)

#TukeyHSD(aov(FvFm~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y',]))

# Panel B: P_max per chl
bargraph.CI(Prey,Pmax_chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y'],,ylim=c(0,15*12.01/44.01))

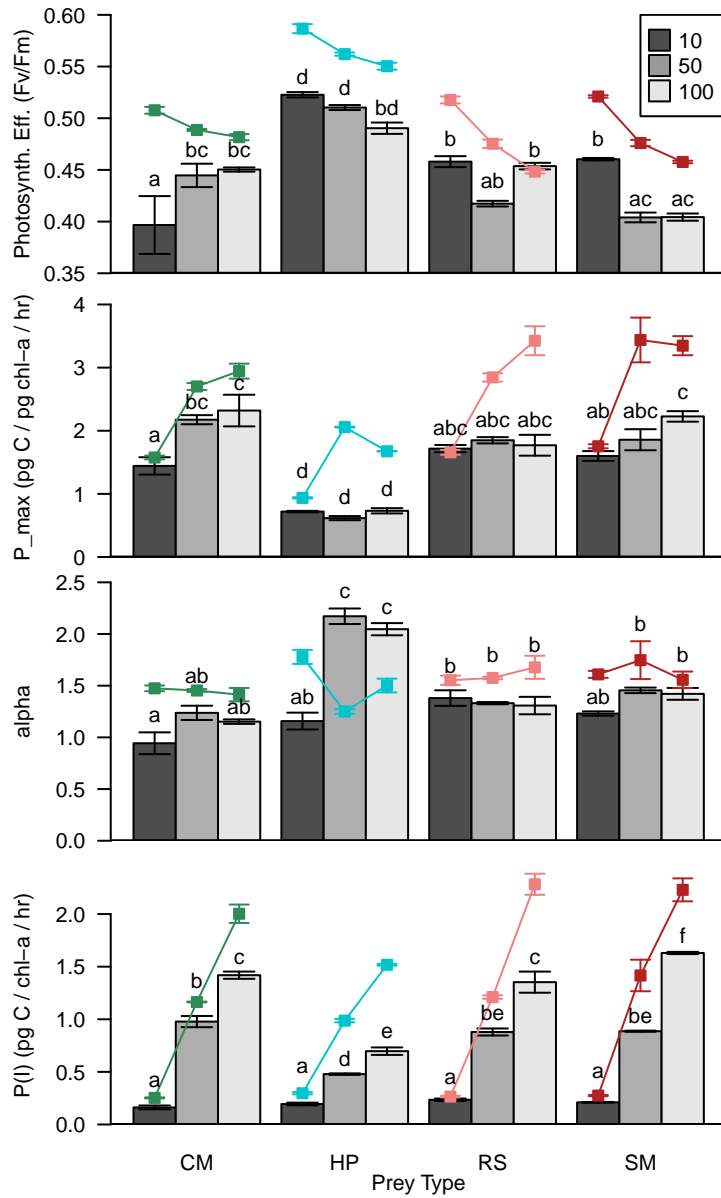
#TukeyHSD(aov(Pmax_chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# Panel C: alpha
bargraph.CI(Prey,a,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y'],,ylim=c(0,2.5),las=1,space=c(0,0))

#TukeyHSD(aov(a~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# Panel D: P(I) per chl
bargraph.CI(Prey,PI_chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y'],,ylim=c(0,9)*12.01/44.01)

#TukeyHSD(aov(PI_chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))
```



Supplementary Figure: Relative photosynthetic capacity (compared to prey)

```
preytypes <- c('CM','HP','RS','SM'); ptcex <- 1.5
#quartz(width=6.28,height=5.44)
par(mar=c(4,4,0.2,1),mfrow=c(2,2))

plot(MC.max[MC.max$Fed=='Y'],$Light,MC.max[MC.max$Fed=='Y'],$relFvFm,pch=21,bg= preycolvec[MC.max[MC.max$Fed=='Y'],$Light])
plot(MC.max[MC.max$Fed=='Y'],$Light,MC.max[MC.max$Fed=='Y'],$rela,pch=21,bg= preycolvec[MC.max[MC.max$Fed=='Y'],$Light])
plot(MC.max[MC.max$Fed=='Y'],$Light,MC.max[MC.max$Fed=='Y'],$relPmax_chl,pch=21,bg= preycolvec[MC.max[MC.max$Fed=='Y'],$Light])
plot(MC.max[MC.max$Fed=='Y'],$Light,MC.max[MC.max$Fed=='Y'],$relPI_chl,pch=21,bg= preycolvec[MC.max[MC.max$Fed=='Y'],$Light])
```

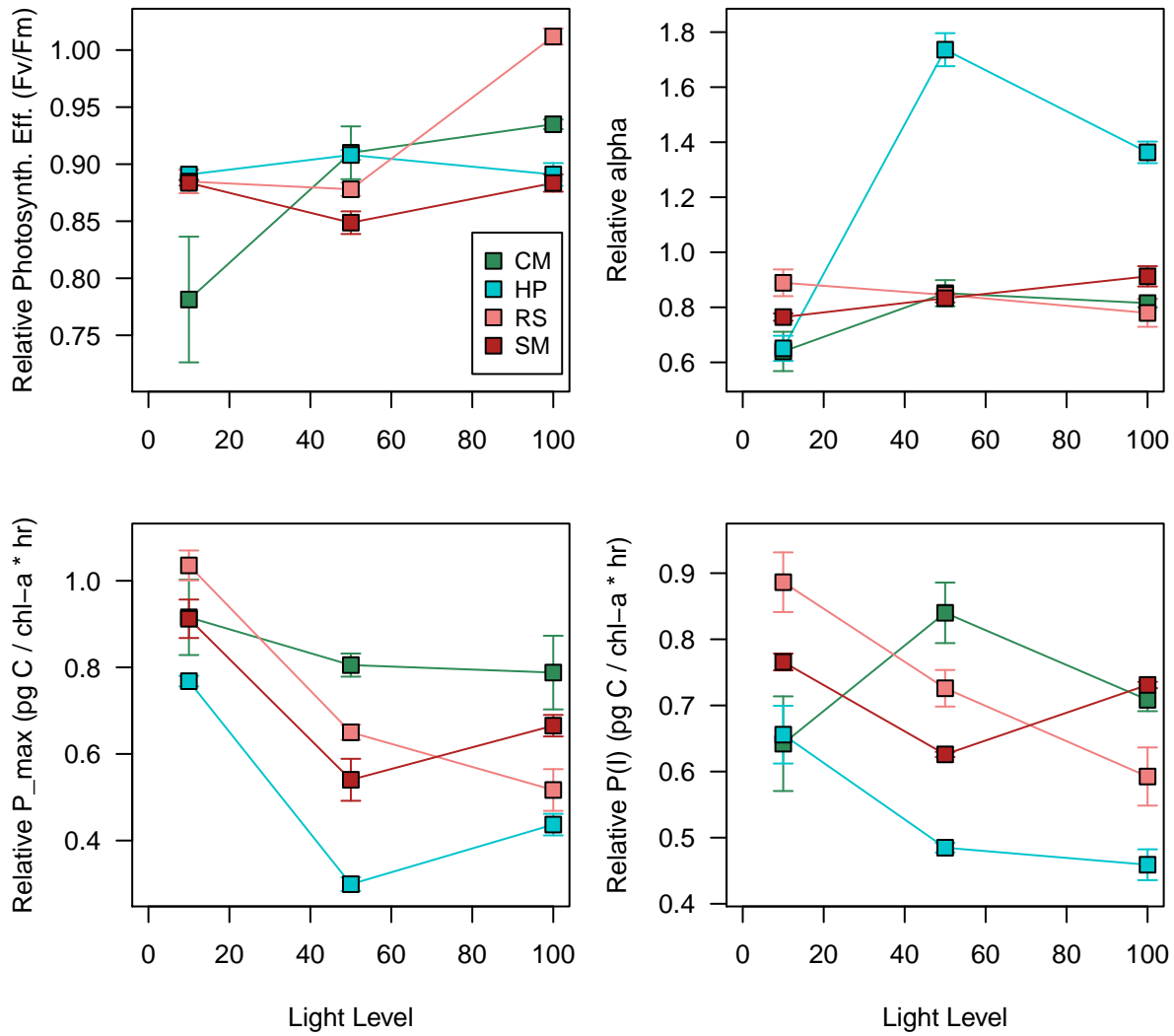


Figure 3: Per-cell plastids, pigment, and C fixation

```
#quartz(height=4.6,width=4.65)
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
par(mar=c(0.5,4,0.5,4))
layout(matrix(c(1,1,1,2,2,2,3,3,3,4)))

bargraph.CI(Prey,plastids,group=Light,data=MC.max[MC.max$Fed=='Y'],legend=FALSE,x.leg=1,y.leg=15,ylim=
#TukeyHSD(aov(plastids~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y']))

# chl-a per cell
bargraph.CI(Prey,chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y'],las=1,ylim=c(0,60),space=c(0,
legend(x = 0.25, y = 55, legend=c('10','50','100'), pch=22,pt.cex=2.5,pt.bg=c('gray30','gray60','gray90
#TukeyHSD(aov(chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y']))

# P(I) per cell
```

```
bargraph.CI(Prey,PI_cell,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y'],las=1,ylim=c(0,170)*12.01,
mtext('Prey P(I) (pg C / crypto / hr)',side=4,line=2,cex=0.7); text(xcoords,c(18,108,118,24,43,43,45,9,
#TukeyHSD(aov(PI_cell~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y'],))
```

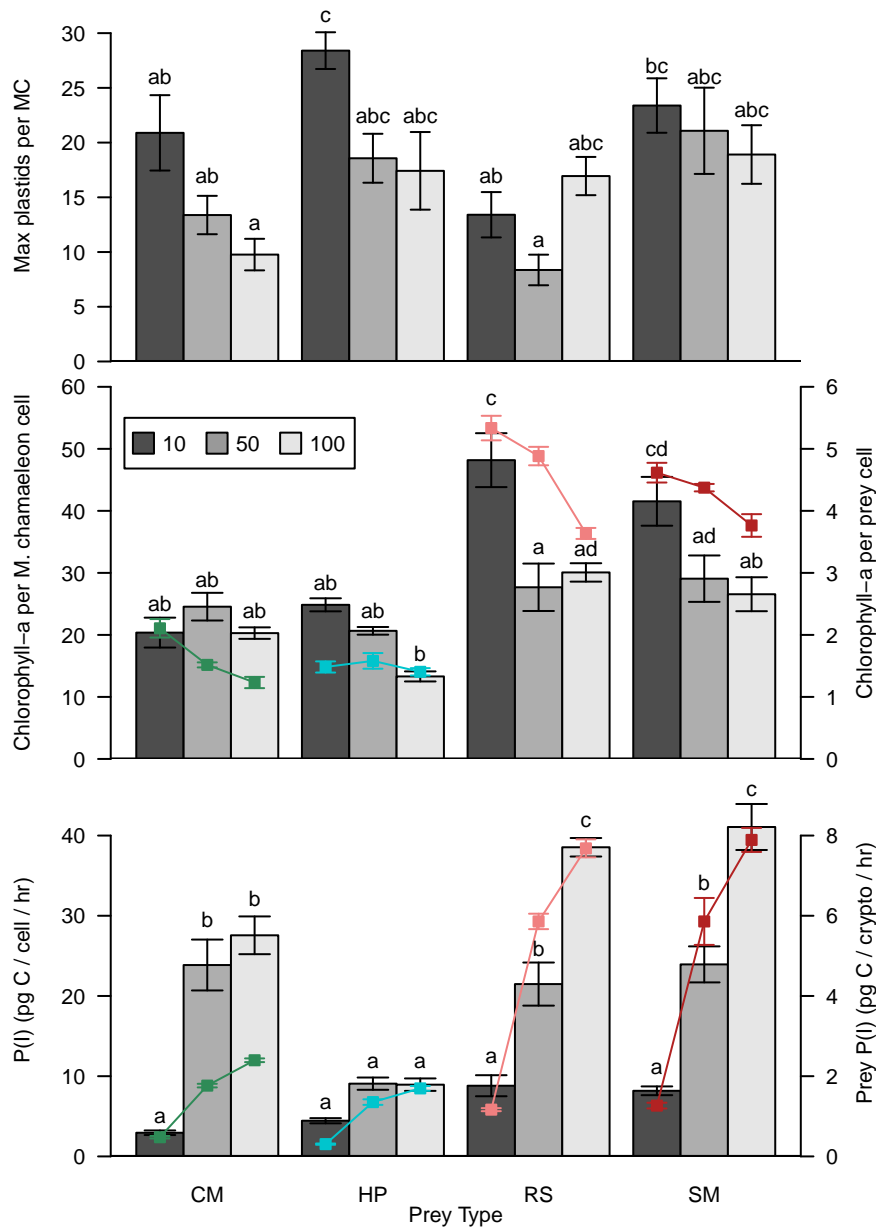


Figure 3, Revised: Per-cell plastids, pigment, and C fixation

```
#quartz(height=4.6,width=4.65)
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
par(mar=c(0.5,4,0.5,4))
layout(matrix(c(1,1,1,2,2,2,3,3,3,4,4,4,5,5,5,6)))
bargraph.CI(Prey,plastids,group=Light,data=MC.max[MC.max$Fed=='Y'],legend=FALSE,x.leg=1,y.leg=15,ylim=
```

```

#TukeyHSD(aov(plastids~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y',]))

# chl-a per cell
bargraph.CI(Prey,chl,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,60),space=c(0,
legend(x = 0.25, y = 55, legend=c('10','50','100'), pch=22,pt.cex=2.5,pt.bg=c('gray30','gray60','gray90
#TukeyHSD(aov(chl~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# P(I) per cell
bargraph.CI(Prey,PI_cell,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,170)*12.01,
mtext('Prey P(I) (pg C / crypto / hr) ',side=4,line=2.2,cex=0.7); text(xcoords,c(18,108,118,24,43,43,45

#TukeyHSD(aov(PI_cell~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

# chl per C
bargraph.CI(Prey,ChlperC,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,90),space=
text(xcoords,c(26,31,24,48,39,28,85,52,52,68,50,55),c('a','ab','a','bc','ab','a','d','bc','c',
#TukeyHSD(aov(ChlperC~as.factor(Light)*Prey,data=MC.max[MC.max$Fed=='Y',]))

# P(I) per C
bargraph.CI(Prey,PI_C,group=as.factor(Light),data=MC.max[MC.max$Fed=='Y',],las=1,ylim=c(0,250)*12.01/44
mtext('Prey P(I) (pg C / crypto / hr) ',side=4,line=2.5,cex=0.7); text(xcoords,c(38,115,128,40,83,73,70

#TukeyHSD(aov(PI_cell~Prey*as.factor(Light),data=MC.max[MC.max$Fed=='Y',]))

```

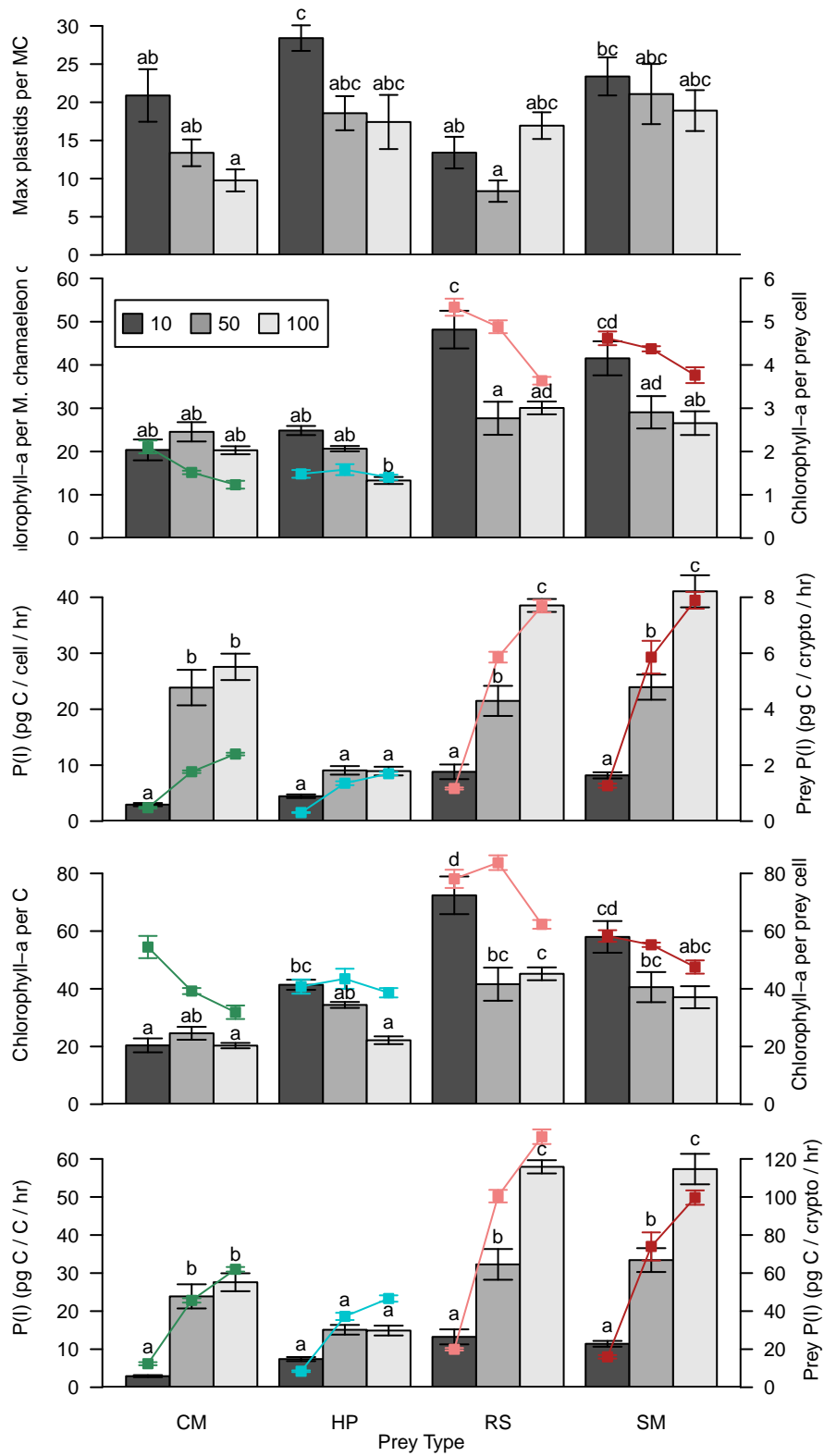


Figure 4: Growth rate and extent

```

growth.summ<-summarySE(data=growth,measurevar='muMC',groupvars=c('Prey','Light','Fed'))
growth$Prey.Light <- paste(growth$Prey,growth$Light,sep='.')
prey.growth.summ <- summarySE(data=growth[growth$Fed=='Y',],measurevar='muPreyCtrl',groupvars=c('Prey',

xcoords <- c(1.2,3.4,5.6)
xcoords2 <- c(.7,1.7,2.9,3.9,5.1,6.1)
#quartz(height=3.5,width=7.5)
par(mar=c(1,1,0.5,0.5))
layout(matrix(c(11,1,1,1,1,2,2,3,3,3,4,4,4,9,9,9,9,9,9,10,5,5,5,6,6,6,7,7,7,8,8,8,9,9,9,9,9),nrow=2,n

# Column 1: Growth Rate
ymax <- 1.2; ymin <- -0.1; bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='CM',],las=1,legend=FALSE,leg.lab=c('Starved'))
bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('Starved'))
bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,leg.lab=c('Starved'))
bargraph.CI(Light,muMC,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=FALSE,leg.lab=c('Starved'))

# Row 2: growth extent
xlabelstr <- '10uE'      50uE      100uE'
ymax <- 12.4; ymin <- 0; bargraph.CI(Light,relincrease,group=Fed,data=growth[growth$Prey=='CM',],las=1,legend=FALSE,leg.lab=c('Starved'))
bargraph.CI(Light,relincrease,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('Starved'))
bargraph.CI(Light, relincrease,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,leg.lab=c('Starved'))
bargraph.CI(Light, relincrease,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=FALSE,leg.lab=c('Starved'))

par(mar=c(4,5,0.1,0.1))
ptcex <- 2

# First panel: growth rate vs. growth extent

lm.all <- lm(growth$relincrease~growth$muMC); summary(lm.all) #signif.; F-stat = 86.4, p-val = 7.616e-16

##
## Call:
## lm(formula = growth$relincrease ~ growth$muMC)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.8268 -1.0467 -0.4266  1.0790  5.4003
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.1771     0.4529   0.391   0.697

```



```

## growth$muMC 13.0391      1.4028    9.295 7.62e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.892 on 70 degrees of freedom
## Multiple R-squared:  0.5524, Adjusted R-squared:  0.546
## F-statistic: 86.4 on 1 and 70 DF,  p-value: 7.616e-14
lm.RS <- lm(relincrease~muMC,data=growth[growth$Prey=='RS',]); summary(lm.RS) #signif.; F-stat = 39.13,

##
## Call:
## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##      "RS", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1669 -1.3449  0.3205  1.3619  3.3652
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.942      1.262  -1.539   0.143
## muMC           21.457      3.430   6.255 1.15e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.951 on 16 degrees of freedom
## Multiple R-squared:  0.7098, Adjusted R-squared:  0.6916
## F-statistic: 39.13 on 1 and 16 DF,  p-value: 1.148e-05
lm.SM <- lm(relincrease~muMC,data=growth[growth$Prey=='SM',]); summary(lm.SM) #signif.; F-stat = 36.33,

##
## Call:
## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##      "SM", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.3789 -0.6495 -0.1635  0.4765  2.4325
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.1947      0.7310  -0.266   0.793
## muMC           13.2977      2.2061   6.028 1.76e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.194 on 16 degrees of freedom
## Multiple R-squared:  0.6943, Adjusted R-squared:  0.6752
## F-statistic: 36.33 on 1 and 16 DF,  p-value: 1.758e-05
lm.CM <- lm(relincrease~muMC,data=growth[growth$Prey=='CM',]); summary(lm.CM) #signif.; F-stat = 138.7,

##
## Call:

```

```

## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##      "CM", ])
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -1.7871 -0.4654 -0.2081  0.5969  2.0592
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.9255     0.3480   2.659  0.0171 *
## muMC          16.1727     1.3733  11.777  2.7e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.054 on 16 degrees of freedom
## Multiple R-squared:  0.8966, Adjusted R-squared:  0.8901
## F-statistic: 138.7 on 1 and 16 DF,  p-value: 2.7e-09
lm.HP <- lm(relincrease~muMC,data=growth[growth$Prey=='HP',]); summary(lm.HP) #signif.; F-stat = 45.33,

##
## Call:
## lm(formula = relincrease ~ muMC, data = growth[growth$Prey ==
##      "HP", ])
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -0.82467 -0.28724  0.00287  0.15622  1.06984
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.5010     0.2923   1.714   0.106
## muMC          5.9977     0.8908   6.733 4.81e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5175 on 16 degrees of freedom
## Multiple R-squared:  0.7391, Adjusted R-squared:  0.7228
## F-statistic: 45.33 on 1 and 16 DF,  p-value: 4.81e-06
plot(growth$muMC,growth$relincrease,pch=c(21,22,24)[as.factor(growth$Light)],bg=c(CMcol,HPcol,RScol,SMcol)

## Warning in arrows(C.summ[, 5], I.summ[, 5] + I.summ$se, C.summ[, 5],
## I.summ[, : zero-length arrow is of indeterminate angle and so skipped
#legend(x = -0.15, y = 12, legend = c('0 uE', '50 uE', '100 uE', 'CM', 'HP', 'RS', 'SM'),cex=ptcex,pt.cex=1.5

```

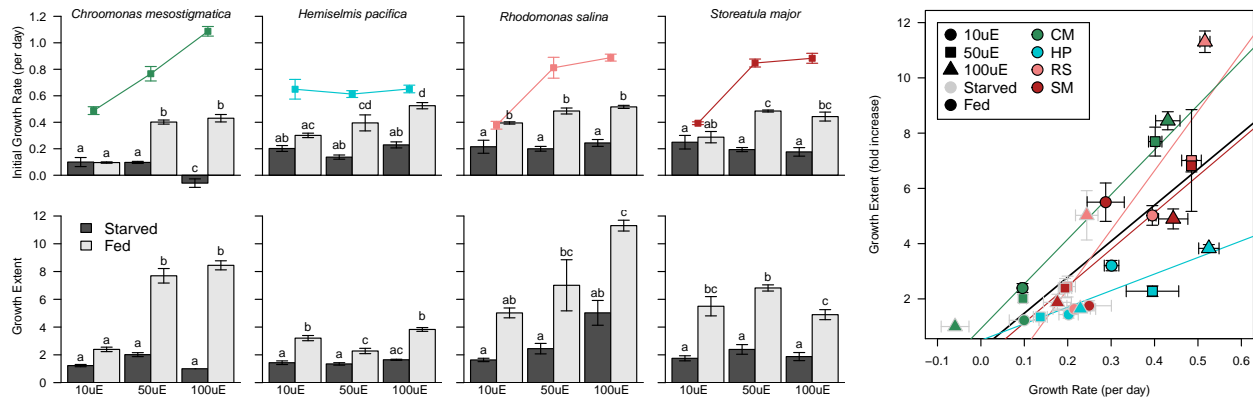


Figure 5: Heterotrophic contributions to growth

```
#layout(matrix(c(1,1,1,2,2,2,8,3,3,3,4,4,4,7,5,5,5,6,6,6,9),nrow=(6*3+3),ncol=1))
layout(matrix(c(1,1,1,2,2,3,3,3,4,4),nrow=2,ncol=5,byrow=TRUE))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)
```

```
# ingestion rate
```

```
par(mar=c(2,4,0.5,0.5))
```

```
bargraph.CI(Prey, ingest_2, group=Light, data=growth[growth$Fed=="Y",], legend=FALSE, x.legend=1, y.legend=15, ylim=c(0,12))
```

```
par(mar=c(4,4,1,0.5))
```

```
# SECOND PLOT: ingestion rate vs growth rate
```

```
lm.all <- lm(growth[growth$Fed=="Y",]$muMC~growth[growth$Fed=="Y",]$ingest_2); summary(lm.all) #signif.
```

```
##
```

```
## Call:
```

```
## lm(formula = growth[growth$Fed == "Y", ]$muMC ~ growth[growth$Fed == "Y", ]$ingest_2)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
```

```
## -0.27035 -0.04367  0.01011  0.07994  0.16933
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)      0.266463    0.042546   6.263 3.93e-07
```

```
## growth[growth$Fed == "Y", ]$ingest_2 0.017805    0.005259   3.386  0.0018
```

```
##
```

```
## (Intercept)          ***
```

```
## growth[growth$Fed == "Y", ]$ingest_2 **
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Residual standard error: 0.1089 on 34 degrees of freedom
```

```
## Multiple R-squared:  0.2522, Adjusted R-squared:  0.2302
```

```
## F-statistic: 11.46 on 1 and 34 DF, p-value: 0.001805
```

```

lm.RS <- lm(muMC~ingest_2,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS) #signif.; F-

##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "RS" &
##     growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.085170 -0.056651  0.008239  0.059667  0.068218
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.459887   0.081843   5.619  0.0008 ***
## ingest_2     0.000672   0.009708   0.069  0.9468
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06338 on 7 degrees of freedom
## Multiple R-squared:  0.000684, Adjusted R-squared:  -0.1421
## F-statistic: 0.004791 on 1 and 7 DF, p-value: 0.9468
lm.SM <- lm(muMC~ingest_2,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM) #signif.; F-

##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "SM" &
##     growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.07256 -0.05838  0.00850  0.05436  0.08521
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.189548   0.067162   2.822  0.0257 *
## ingest_2     0.020717   0.006088   3.403  0.0114 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06686 on 7 degrees of freedom
## Multiple R-squared:  0.6233, Adjusted R-squared:  0.5694
## F-statistic: 11.58 on 1 and 7 DF, p-value: 0.0114
lm.CM <- lm(muMC~ingest_2,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM) #signif.; F-

##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "CM" &
##     growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.21576 -0.15231  0.01321  0.11083  0.16924
##

```

```
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.18688    0.11165   1.674   0.138
## ingest_2     0.02215    0.01782   1.243   0.254
##
## Residual standard error: 0.1578 on 7 degrees of freedom
## Multiple R-squared:  0.1808, Adjusted R-squared:  0.06382
## F-statistic: 1.545 on 1 and 7 DF,  p-value: 0.2538

lm.HP <- lm(muMC~ingest_2,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP) #signif.; F-

##
## Call:
## lm(formula = muMC ~ ingest_2, data = growth[growth$Prey == "HP" &
##       growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.094714 -0.028945  0.006322  0.040034  0.071321
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.12162    0.06364   1.911  0.09763 .
## ingest_2     0.05503    0.01166   4.720  0.00216 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0593 on 7 degrees of freedom
## Multiple R-squared:  0.7609, Adjusted R-squared:  0.7267
## F-statistic: 22.27 on 1 and 7 DF,  p-value: 0.002159

plot(growth[growth$Fed=='Y',]$ingest_2,growth[growth$Fed=='Y',]$muMC,las=1,pch=c(21,22,24)[as.factor(growth$Prey)],
C.summ <- summarySE(data=growth[growth$Fed=='Y',],measurevar='muMC',groupvars=c('Light','Prey')); I.summary(C.summ)

legend(13.1,0.29,legend=c('10uE','50uE','100uE'),pch=c(21,22,24),pt.cex=ptcex,pt.bg='black',col='black')

# linear scale: prey per initial MC
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,(PreyperMC),group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,names=c('10uE','50uE','100uE'))

# FOURTH PLOT: total ingestion vs growth extent

par(mar=c(4,4,1,0.5))
growth.y <- growth[growth$Fed=='Y',]
lm.all <- lm(growth.y$relincrease~log(growth.y$PreyperMC)); summary(lm.all) #signif.; F-stat = 8.4, p-value = 0.014

##
## Call:
## lm(formula = growth.y$relincrease ~ log(growth.y$PreyperMC))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```

## -3.4740 -1.2625 -0.4977  0.6485  6.5826
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.6685      1.7857   0.374  0.71047
## log(growth.y$PreyperMC)  1.4408      0.4971   2.898  0.00652 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.511 on 34 degrees of freedom
## Multiple R-squared:  0.1981, Adjusted R-squared:  0.1745
## F-statistic:  8.4 on 1 and 34 DF,  p-value: 0.006525
lm.RS.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='RS'&growth.y$Fed=='Y',]); summary

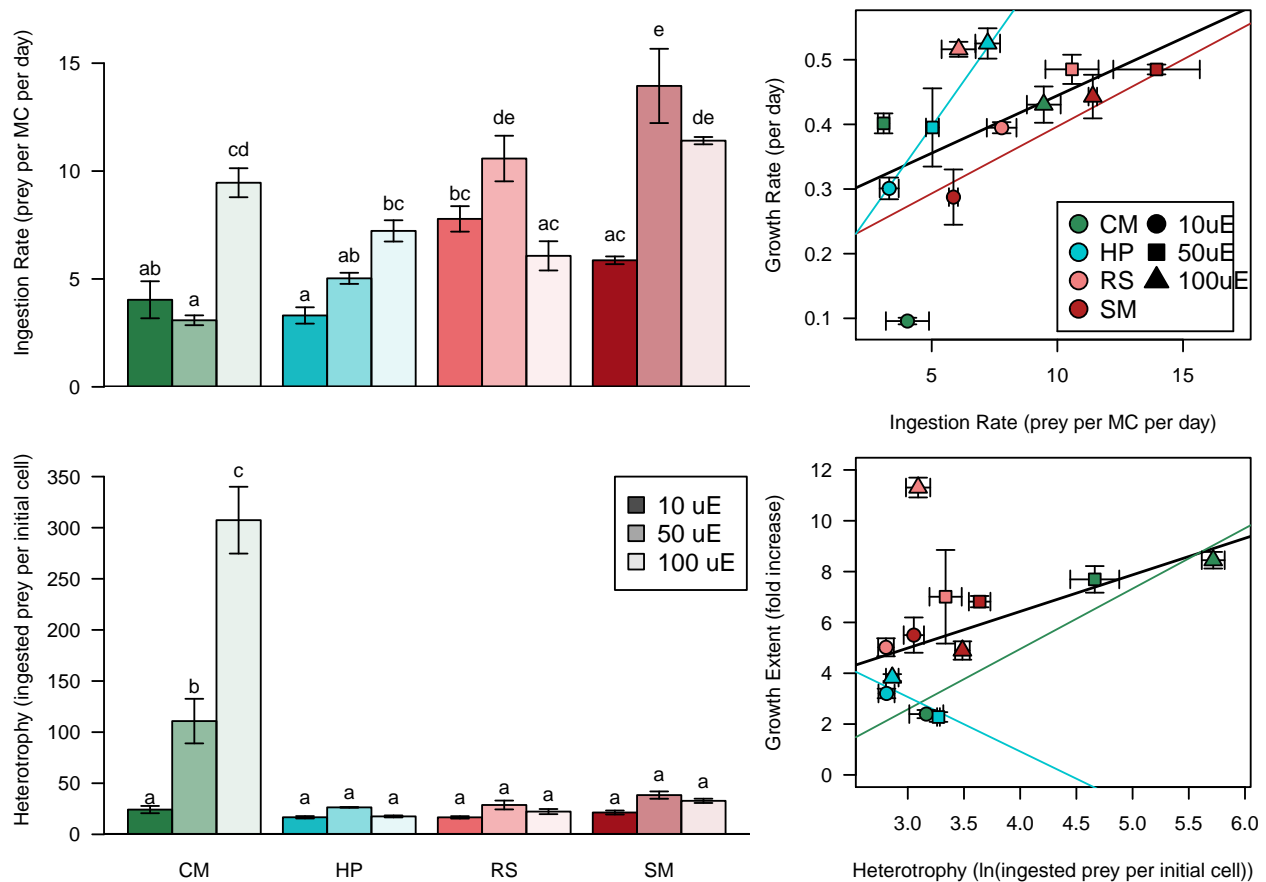
##
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
## "RS" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.0784 -1.4995 -0.8877  2.9664  4.1790
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -9.476      11.599  -0.817   0.441
## log(PreyperMC)    5.606       3.754   1.493   0.179
##
## Residual standard error: 3.016 on 7 degrees of freedom
## Multiple R-squared:  0.2416, Adjusted R-squared:  0.1333
## F-statistic:  2.23 on 1 and 7 DF,  p-value: 0.179
lm.SM.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='SM'&growth.y$Fed=='Y',]); summary

##
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
## "SM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.45464 -0.81082  0.05431  0.65520  1.45024
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.056       4.534   0.233   0.823
## log(PreyperMC)    1.380       1.332   1.036   0.335
##
## Residual standard error: 1.1 on 7 degrees of freedom
## Multiple R-squared:  0.133, Adjusted R-squared:  0.009104
## F-statistic: 1.073 on 1 and 7 DF,  p-value: 0.3346
lm.CM.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='CM'&growth.y$Fed=='Y',]); summary

##

```

```
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
## "CM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.96250 -0.71021 -0.18499 -0.08223  1.92060
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -4.5418     1.6693  -2.721 0.029730 *
## log(PreyperMC)  2.3742     0.3597   6.601 0.000304 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.158 on 7 degrees of freedom
## Multiple R-squared:  0.8616, Adjusted R-squared:  0.8418
## F-statistic: 43.57 on 1 and 7 DF,  p-value: 0.0003041
lm.HP.f <- lm(relincrease~log(PreyperMC),data=growth.y[growth.y$Prey=='HP'&growth.y$Fed=='Y',]); summary(lm.HP.f)
##
## Call:
## lm(formula = relincrease ~ log(PreyperMC), data = growth.y[growth.y$Prey ==
## "HP" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8070 -0.2609 -0.0068  0.2690  0.7411
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     9.4956     2.5353   3.745 0.00721 **
## log(PreyperMC)  -2.1434     0.8479  -2.528 0.03936 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5596 on 7 degrees of freedom
## Multiple R-squared:  0.4772, Adjusted R-squared:  0.4025
## F-statistic:  6.39 on 1 and 7 DF,  p-value: 0.03936
plot(log(as.numeric(as.character(growth.y$PreyperMC))),growth.y$relincrease,pch=c(21,22,24)[as.factor(growth.y$Prey)],col=c("red","green","blue"))
```



```
#legend(1050,12.2,legend=c('CM','HP','RS','SM'),pch=21,pt.cex=pt.cex,pt.bg=preycolvec,bty='n'); arrows(c
```

Figure 5, revision: Heterotrophic contributions to growth

```
#layout(matrix(c(1,1,1,2,2,2,8,3,3,3,4,4,4,7,5,5,5,6,6,6,9),nrow=(6*3+3),ncol=1))
layout(matrix(c(1,1,1,2,2,3,3,3,4,4),nrow=2,ncol=5,byrow=TRUE))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

# ingestion rate
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,ingest_2,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,x.leg=1,y.leg=15,ylim=)

par(mar=c(4,4,1,0.5))

# SECOND PLOT: ingestion rate vs growth rate
# Revision: convert to per carbon
carbon$Prey.Rep <- paste(carbon$Prey,carbon$Rep,sep='.')
carbon$Sp.Rep <- paste(carbon$Species,carbon$Rep,sep='.')
growth$Prey.Rep <- paste(growth$Prey,growth$Rep,sep='.')
growth$MC.C <- carbon[carbon$Species=='MC',]$ngC_cell[match(growth$Prey.Rep,carbon[carbon$Species=='MC'
growth$prey.C <- carbon[carbon$Species!='MC',]$ngC_cell[match(growth$Prey.Rep,carbon[carbon$Species!='MC'
```



```

growth$preyCperMCperday <- growth$ingest_2*growth$prey.C/growth$MC.C
growth$heterotrophy.C <- growth$PreyperMC*growth$prey.C/growth$MC.C

lm.all <- lm(growth[growth$Fed=='Y',]$muMC~growth[growth$Fed=='Y',]$preyCperMCperday); summary(lm.all)

##
## Call:
## lm(formula = growth[growth$Fed == "Y", ]$muMC ~ growth[growth$Fed ==
##      "Y", ]$preyCperMCperday)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.25597 -0.06217  0.02526  0.07555  0.17508
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept)      0.32865    0.03136   10.48
## growth[growth$Fed == "Y", ]$preyCperMCperday  0.11187    0.04098    2.73
##              Pr(>|t|)
## (Intercept)      3.46e-12 ***
## growth[growth$Fed == "Y", ]$preyCperMCperday  0.00996 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1141 on 34 degrees of freedom
## Multiple R-squared:  0.1798, Adjusted R-squared:  0.1557
## F-statistic: 7.454 on 1 and 34 DF,  p-value: 0.009955

lm.RS <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS) #n.s

##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##      "RS" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.085490 -0.059006  0.004134  0.052806  0.070208
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.45052    0.06457   6.977 0.000216 ***
## preyCperMCperday  0.02013    0.08278   0.243 0.814840
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06314 on 7 degrees of freedom
## Multiple R-squared:  0.008377, Adjusted R-squared: -0.1333
## F-statistic: 0.05914 on 1 and 7 DF,  p-value: 0.8148

lm.SM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM) #sig

##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==

```

```
##      "SM" & growth$Fed == "Y", ])
```

```
##
```

```
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.089937	-0.058651	-0.009645	0.053621	0.085126

```
##
```

```
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	0.21793	0.06763	3.222	0.0146 *
preyCperMCperday	0.16037	0.05410	2.964	0.0210 *

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Residual standard error: 0.07253 on 7 degrees of freedom
```

```
## Multiple R-squared:  0.5566, Adjusted R-squared:  0.4932
```

```
## F-statistic: 8.786 on 1 and 7 DF,  p-value: 0.02098
```

```
lm.CM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM) #n.s
```

```
##
```

```
## Call:
```

```
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
```

```
##      "CM" & growth$Fed == "Y", ])
```

```
##
```

```
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.2038	-0.1670	0.0300	0.1156	0.1690

```
##
```

```
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	0.1974	0.1066	1.852	0.106
preyCperMCperday	0.5200	0.4302	1.209	0.266

```
##
```

```
## Residual standard error: 0.1585 on 7 degrees of freedom
```

```
## Multiple R-squared:  0.1727, Adjusted R-squared:  0.0545
```

```
## F-statistic: 1.461 on 1 and 7 DF,  p-value: 0.266
```

```
lm.HP <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP) #sig
```

```
##
```

```
## Call:
```

```
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
```

```
##      "HP" & growth$Fed == "Y", ])
```

```
##
```

```
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.095104	-0.023532	0.002273	0.042511	0.052887

```
##
```

```
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	0.12936	0.05598	2.311	0.05412 .
preyCperMCperday	0.88395	0.16847	5.247	0.00119 **

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```

## Residual standard error: 0.0546 on 7 degrees of freedom
## Multiple R-squared:  0.7973, Adjusted R-squared:  0.7683
## F-statistic: 27.53 on 1 and 7 DF,  p-value: 0.00119

plot(growth[growth$Fed=='Y'],$preyCperMCperday,growth[growth$Fed=='Y'],$muMC,las=1,pch=c(21,22,24)[as.f
C.summ <- summarySE(data=growth[growth$Fed=='Y'],measurevar='muMC',groupvars=c('Light','Prey')); I.sum

legend(1.5,0.29,legend=c('10uE','50uE','100uE'),pch=c(21,22,24),pt.cex=ptcex,pt.bg='black',col='black',l

# linear scale: prey per initial MC
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,(PreyperMC),group=Light,data=growth[growth$Fed=='Y'],legend=FALSE,err.width=0.05,names

# FOURTH PLOT: total ingestion vs growth extent

par(mar=c(4,4,1,0.5))
growth.y <- growth[growth$Fed=='Y',]
lm.all <- lm(growth.y$relincrease~log(growth.y$heterotrophy.C)); summary(lm.all) #signif.; F-stat = 8.4

##
## Call:
## lm(formula = growth.y$relincrease ~ log(growth.y$heterotrophy.C))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.0097 -1.0832 -0.4442  0.0672  6.0001
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.9082     0.5595   6.986 4.66e-08 ***
## log(growth.y$heterotrophy.C)  2.1809     0.5048   4.320 0.000128 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.253 on 34 degrees of freedom
## Multiple R-squared:  0.3544, Adjusted R-squared:  0.3354
## F-statistic: 18.66 on 1 and 34 DF,  p-value: 0.0001283

lm.RS.f <- lm(relincrease~log(heterotrophy.C),data=growth.y[growth.y$Prey=='RS'&growth.y$Fed=='Y',]); s

##
## Call:
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "RS" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.9145 -2.3739 -0.1336  2.7505  4.2343
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.890      2.185   2.238  0.0602 .

```

```

## log(heterotrophy.C)    4.434      2.977   1.490   0.1799
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.018 on 7 degrees of freedom
## Multiple R-squared:  0.2407, Adjusted R-squared:  0.1322
## F-statistic: 2.219 on 1 and 7 DF,  p-value: 0.1799
lm.SM.f <- lm(relincrease~log(heterotrophy.C),data=growth.y[growth.y$Prey=='SM'&growth.y$Fed=='Y',]); s

##
## Call:
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "SM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5741 -0.9955  0.1905  0.8409  1.3864
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         4.217      1.657   2.544  0.0384 *
## log(heterotrophy.C)   1.270      1.348   0.942  0.3777
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.113 on 7 degrees of freedom
## Multiple R-squared:  0.1125, Adjusted R-squared: -0.01434
## F-statistic: 0.8869 on 1 and 7 DF,  p-value: 0.3777
lm.CM.f <- lm(relincrease~log(heterotrophy.C),data=growth.y[growth.y$Prey=='CM'&growth.y$Fed=='Y',]); s

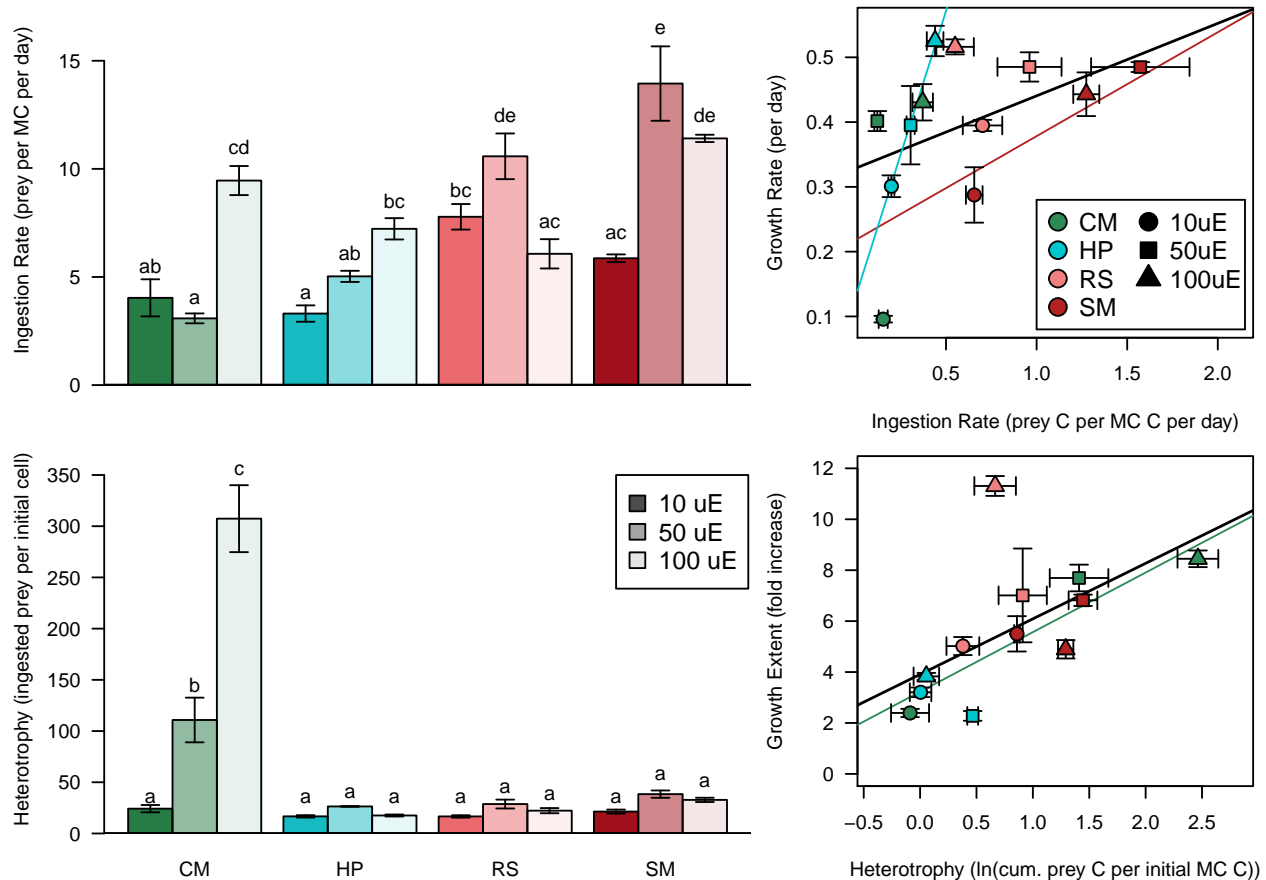
##
## Call:
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "CM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.09514 -0.70175 -0.09685  0.09738  1.93986
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         3.2257      0.5928   5.441 0.000965 ***
## log(heterotrophy.C)   2.3409      0.3560   6.576 0.000311 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.161 on 7 degrees of freedom
## Multiple R-squared:  0.8607, Adjusted R-squared:  0.8408
## F-statistic: 43.25 on 1 and 7 DF,  p-value: 0.0003111
lm.HP.f <- lm(relincrease~log(heterotrophy.C),data=growth.y[growth.y$Prey=='HP'&growth.y$Fed=='Y',]); s

##
## Call:

```

```
## lm(formula = relincrease ~ log(heterotrophy.C), data = growth.y[growth.y$Prey ==
## "HP" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.75770 -0.36393 -0.07023  0.48471  0.89482
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.3804     0.2635  12.828 4.06e-06 ***
## log(heterotrophy.C) -1.5767     0.8801  -1.791   0.116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6409 on 7 degrees of freedom
## Multiple R-squared:  0.3143, Adjusted R-squared:  0.2164
## F-statistic: 3.209 on 1 and 7 DF, p-value: 0.1163
```

```
plot(log(as.numeric(as.character(growth.y$heterotrophy.C))),growth.y$relincrease,pch=c(21,22,24)[as.fact
```



```
#legend(1050,12.2,legend=c('CM','HP','RS','SM'),pch=21,pt.cex=ptcex,pt.bg=preycolvec,bty='n'); arrows(c
```

Figure 5, revision 2: Heterotrophic contributions to growth, linear heterotrophy

```

#layout(matrix(c(1,1,1,2,2,2,8,3,3,3,4,4,4,7,5,5,5,6,6,6,9),nrow=(6*3+3),ncol=1))
layout(matrix(c(1,1,1,2,2,3,3,3,4,4),nrow=2,ncol=5,byrow=TRUE))
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

# ingestion rate
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,ingest_2,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,x.leg=1,y.leg=15,ylim=)

par(mar=c(4,4,1,0.5))

# SECOND PLOT: ingestion rate vs growth rate
# Revision: convert to per carbon
carbon$Prey.Rep <- paste(carbon$Prey,carbon$Rep,sep='.')
carbon$Sp.Rep <- paste(carbon$Species,carbon$Rep,sep='.')
growth$Prey.Rep <- paste(growth$Prey,growth$Rep,sep='.')
growth$MC.C <- carbon[carbon$Species=='MC',]$nC_cell[match(growth$Prey.Rep,carbon[carbon$Species=='MC'
growth$prey.C <- carbon[carbon$Species!='MC',]$nC_cell[match(growth$Prey.Rep,carbon[carbon$Species!='MC'

growth$preyCperMCperday <- growth$ingest_2*growth$prey.C/growth$MC.C
growth$heterotrophy.C <- growth$PreyperMC*growth$prey.C/growth$MC.C

lm.all <- lm(growth[growth$Fed=='Y',]$muMC~growth[growth$Fed=='Y',]$preyCperMCperday); summary(lm.all)

##
## Call:
## lm(formula = growth[growth$Fed == "Y", ]$muMC ~ growth[growth$Fed ==
##      "Y", ]$preyCperMCperday)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.25597 -0.06217  0.02526  0.07555  0.17508
##
## Coefficients:
##                                Estimate Std. Error t value
## (Intercept)                   0.32865    0.03136   10.48
## growth[growth$Fed == "Y", ]$preyCperMCperday 0.11187    0.04098    2.73
##                                Pr(>|t|)
## (Intercept)                   3.46e-12 ***
## growth[growth$Fed == "Y", ]$preyCperMCperday 0.00996 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1141 on 34 degrees of freedom
## Multiple R-squared:  0.1798, Adjusted R-squared:  0.1557
## F-statistic: 7.454 on 1 and 34 DF,  p-value: 0.009955

lm.RS <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS) #n.s

##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##      "RS" & growth$Fed == "Y", ])

```

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.085490 -0.059006  0.004134  0.052806  0.070208
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.45052    0.06457   6.977 0.000216 ***
## preyCperMCperday 0.02013    0.08278   0.243 0.814840
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06314 on 7 degrees of freedom
## Multiple R-squared:  0.008377, Adjusted R-squared:  -0.1333
## F-statistic: 0.05914 on 1 and 7 DF, p-value: 0.8148
lm.SM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM) #sig

##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##      "SM" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.089937 -0.058651 -0.009645  0.053621  0.085126
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.21793    0.06763   3.222  0.0146 *
## preyCperMCperday 0.16037    0.05410   2.964  0.0210 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07253 on 7 degrees of freedom
## Multiple R-squared:  0.5566, Adjusted R-squared:  0.4932
## F-statistic: 8.786 on 1 and 7 DF, p-value: 0.02098
lm.CM <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM) #n.s

##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##      "CM" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.2038 -0.1670  0.0300  0.1156  0.1690
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.1974    0.1066   1.852  0.106
## preyCperMCperday 0.5200    0.4302   1.209  0.266
##
## Residual standard error: 0.1585 on 7 degrees of freedom
```

```
## Multiple R-squared:  0.1727, Adjusted R-squared:  0.0545
## F-statistic: 1.461 on 1 and 7 DF,  p-value: 0.266

lm.HP <- lm(muMC~preyCperMCperday,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP) #sig

##
## Call:
## lm(formula = muMC ~ preyCperMCperday, data = growth[growth$Prey ==
##      "HP" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.095104 -0.023532  0.002273  0.042511  0.052887
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.12936    0.05598   2.311  0.05412 .
## preyCperMCperday 0.88395    0.16847   5.247  0.00119 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0546 on 7 degrees of freedom
## Multiple R-squared:  0.7973, Adjusted R-squared:  0.7683
## F-statistic: 27.53 on 1 and 7 DF,  p-value: 0.00119

plot(growth[growth$Fed=='Y',]$preyCperMCperday,growth[growth$Fed=='Y',]$muMC,las=1,pch=c(21,22,24)[as.f
C.summ <- summarySE(data=growth[growth$Fed=='Y',],measurevar='muMC',groupvars=c('Light','Prey')); I.sum

legend(1.5,0.29,legend=c('10uE','50uE','100uE'),pch=c(21,22,24),pt.cex=ptcex,pt.bg='black',col='black',

# linear scale: prey per initial MC
par(mar=c(2,4,0.5,0.5))
bargraph.CI(Prey,(PreyperMC),group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,names

# FOURTH PLOT: total ingestion vs growth extent

par(mar=c(4,4,1,0.5))
growth.y <- growth[growth$Fed=='Y',]
lm.all <- lm(growth.y$relincrease~(growth.y$heterotrophy.C)); summary(lm.all) #signif.; F-stat = 9.359,

##
## Call:
## lm(formula = growth.y$relincrease ~ (growth.y$heterotrophy.C))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1811 -1.6836 -0.5064  0.5715  6.4918
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.4469    0.5822   7.638 7.08e-09 ***
## growth.y$heterotrophy.C  0.4003    0.1309   3.059  0.00431 **
```



```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.483 on 34 degrees of freedom
## Multiple R-squared:  0.2158, Adjusted R-squared:  0.1928
## F-statistic: 9.359 on 1 and 34 DF,  p-value: 0.004308
lm.RS.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='RS'&growth.y$Fed=='Y',]); summa

##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "RS" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6741 -2.3507 -0.6151  2.8925  4.1745
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.549      2.954   1.201   0.269
## heterotrophy.C    2.079      1.366   1.522   0.172
##
## Residual standard error: 3.002 on 7 degrees of freedom
## Multiple R-squared:  0.2487, Adjusted R-squared:  0.1413
## F-statistic: 2.317 on 1 and 7 DF,  p-value: 0.1718
lm.SM.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='SM'&growth.y$Fed=='Y',]); summa

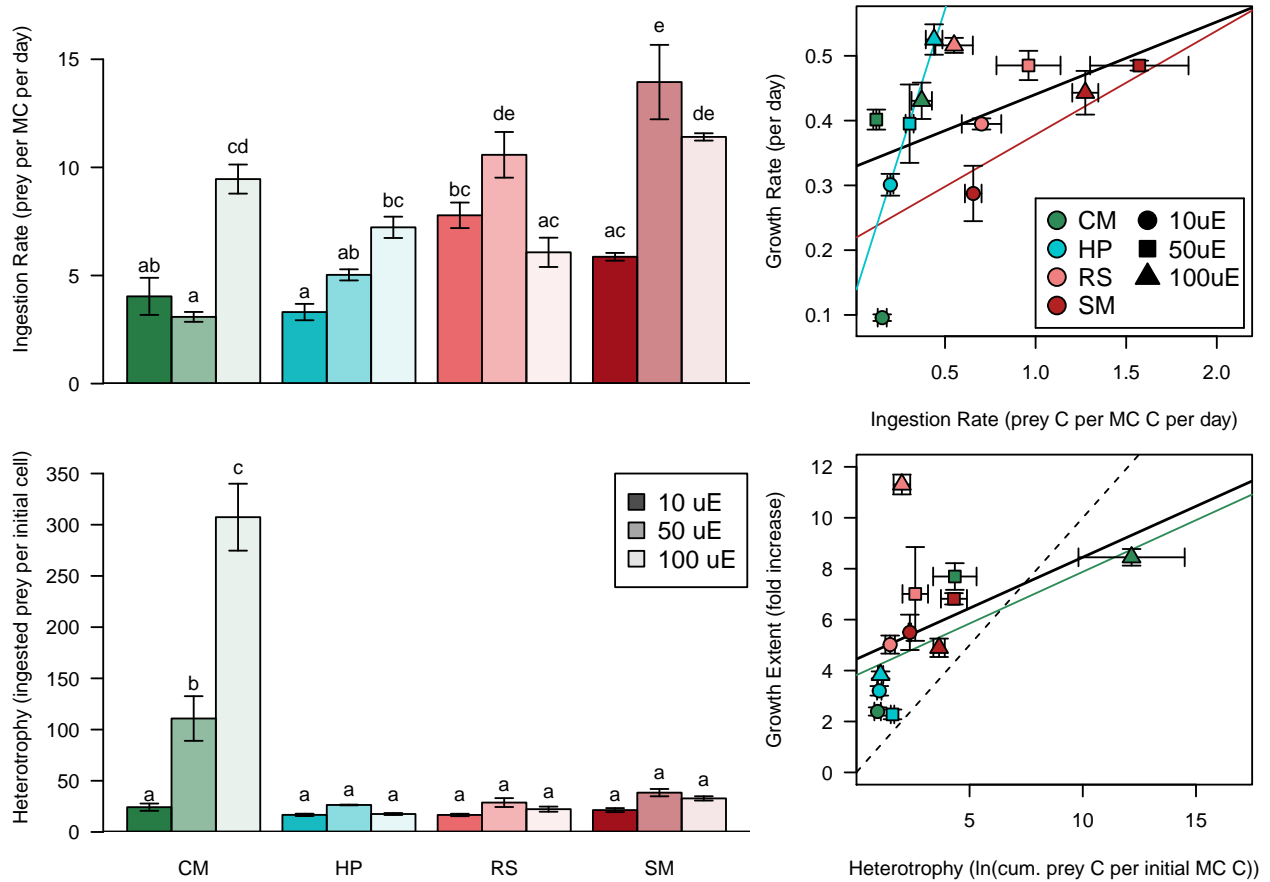
##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "SM" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5751 -0.9955  0.2146  0.6647  1.3919
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.3340      1.3600   3.187   0.0153 *
## heterotrophy.C    0.4079      0.3806   1.072   0.3194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.095 on 7 degrees of freedom
## Multiple R-squared:  0.1409, Adjusted R-squared:  0.01821
## F-statistic: 1.148 on 1 and 7 DF,  p-value: 0.3194
lm.CM.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='CM'&growth.y$Fed=='Y',]); summa

##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "CM" & growth.y$Fed == "Y", ])
##

```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9497 -1.8459  0.1185  1.1614  2.7263
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.8178      1.0203   3.742  0.00725 **
## heterotrophy.C    0.4059      0.1316   3.085  0.01768 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.025 on 7 degrees of freedom
## Multiple R-squared:  0.5763, Adjusted R-squared:  0.5157
## F-statistic:  9.52 on 1 and 7 DF,  p-value: 0.01768
lm.HP.f <- lm(relincrease~(heterotrophy.C),data=growth.y[growth.y$Prey=='HP'&growth.y$Fed=='Y',]); summar

##
## Call:
## lm(formula = relincrease ~ (heterotrophy.C), data = growth.y[growth.y$Prey ==
##      "HP" & growth.y$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.70989 -0.39720 -0.06457  0.43601  0.85154
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.8143      0.8681   5.546 0.000864 ***
## heterotrophy.C  -1.3936      0.6874  -2.027 0.082224 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6143 on 7 degrees of freedom
## Multiple R-squared:  0.37, Adjusted R-squared:  0.28
## F-statistic:  4.11 on 1 and 7 DF,  p-value: 0.08222
plot((as.numeric(as.character(growth.y$heterotrophy.C))),growth.y$relincrease,pch=c(21,22,24)[as.factor
```



*#legend(1050,12.2,legend=c('CM','HP','RS','SM'),pch=21,pt.cex=pt.cex,pt.bg=preycolvec,bty='n'); arrows(c*

**Figure 6: Photosynthetic contributions to growth**

```
layout(matrix(c(8,1,2,3,4,rep(7,3),9,5,5,5,5,rep(7,3),10,6,6,6,6,rep(7,3)),nrow=3,ncol=8,byrow=TRUE));

growth$C.fixed3 <- growth$C.fixed2/1000 # convert from pg to ng
growth$C.per.prey <- growth$C.fixed2/growth$TotPreyCons

xcoords <- c(1.2,3.4,5.6)
xcoords2 <- c(.7,1.7,2.9,3.9,5.1,6.1)
#quartz(height=3.5,width=7.5)
par(mar=c(1,1,0.5,0.5))
#layout(matrix(c(7,1,1,1,2,2,3,3,3,4,4,4,rep(6,6),8,rep(5,3*4),rep(6,6)),nrow=2,ncol=19,byrow=TRUE))

# Row 1: Photosynthate
ymax <- 50*12.01/44.01; ymin <- 0; bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='CM',])

bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('Star'))

bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,ylim=c(ymin,ymax))
```

```

bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=TRUE,leg.lab=c('Starv

# Second row: fold difference
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

bargraph.CI(Prey,C.fixed2/abs(deltaCfixed-C.fixed2),group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,

#TukeyHSD(aov(C.fixed2/abs(deltaCfixed-C.fixed2)~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# Third row: Carbon fixed per prey ingested
bargraph.CI(Prey,C.per.prey,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,las=3

#TukeyHSD(aov(C.per.prey~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# FOURTH PLOT: total photosynthate vs growth extent
par(mar=c(4,5,.5,0.5))

lm.all <- lm(growth$relincrease~growth$C.fixed3); summary(lm.all) #signif.; F-stat = 363.6, p-val = < 2

##
## Call:
## lm(formula = growth$relincrease ~ growth$C.fixed3)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7400 -0.7034 -0.2552  0.6855  3.4925
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.46273     0.18230   8.024 1.65e-11 ***
## growth$C.fixed3  0.73044     0.03814  19.152 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.132 on 70 degrees of freedom
## Multiple R-squared:  0.8397, Adjusted R-squared:  0.8374
## F-statistic: 366.8 on 1 and 70 DF,  p-value: < 2.2e-16
lm.RS.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.RS.f) #

##
## Call:
## lm(formula = relinincrease ~ C.fixed3, data = growth[growth$Prey ==
##      "RS" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.58623 -0.24859  0.08797  0.55830  1.53320
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.59415     0.75984   3.414 0.011225 *

```

```

## C.fixed3      0.76203      0.09752      7.814 0.000106 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.111 on 7 degrees of freedom
## Multiple R-squared:  0.8972, Adjusted R-squared:  0.8825
## F-statistic: 61.06 on 1 and 7 DF,  p-value: 0.0001059
lm.RS.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='RS'&growth$Fed=='N',]); summary(lm.RS.n) #

##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
## "RS" & growth$Fed == "N", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.60262 -0.35354 -0.06898  0.27792  0.72256
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.19688     0.25227   4.744  0.0021 **
## C.fixed3      0.62499     0.06484   9.640 2.72e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4955 on 7 degrees of freedom
## Multiple R-squared:  0.9299, Adjusted R-squared:  0.9199
## F-statistic: 92.92 on 1 and 7 DF,  p-value: 2.724e-05
lm.SM.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.SM.f) #

##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
## "SM" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.40307 -1.20669  0.05384  0.96935  1.36544
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.36265     0.95182   5.634 0.000787 ***
## C.fixed3      0.07546     0.17473   0.432 0.678818
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.166 on 7 degrees of freedom
## Multiple R-squared:  0.02595, Adjusted R-squared: -0.1132
## F-statistic: 0.1865 on 1 and 7 DF,  p-value: 0.6788
lm.SM.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='SM'&growth$Fed=='N',]); summary(lm.SM.n) #

##
## Call:

```

```

## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##      "SM" & growth$Fed == "N", ])
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -0.62041 -0.35385 -0.01644  0.24170  0.87923
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.7073     0.3184   5.362  0.00105 **
## C.fixed3       0.1767     0.1596   1.107  0.30491
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5083 on 7 degrees of freedom
## Multiple R-squared:  0.149, Adjusted R-squared:  0.02739
## F-statistic: 1.225 on 1 and 7 DF, p-value: 0.3049
lm.CM.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM.f) #

##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##      "CM" & growth$Fed == "Y", ])
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -0.55407 -0.29453  0.04931  0.17498  0.76372
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2.24560     0.24109   9.314 3.41e-05 ***
## C.fixed3       0.57254     0.02887  19.832 2.07e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4114 on 7 degrees of freedom
## Multiple R-squared:  0.9825, Adjusted R-squared:  0.98
## F-statistic: 393.3 on 1 and 7 DF, p-value: 2.072e-07
lm.CM.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='CM'&growth$Fed=='N',]); summary(lm.CM.n) #

##
## Call:
## lm(formula = relincrease ~ C.fixed3, data = growth[growth$Prey ==
##      "CM" & growth$Fed == "N", ])
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -0.5348 -0.5008  0.1913  0.2208  0.5839
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.9822     0.3281   2.994  0.0201 *
## C.fixed3       0.8641     0.5840   1.480  0.1825

```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4506 on 7 degrees of freedom
## Multiple R-squared:  0.2383, Adjusted R-squared:  0.1294
## F-statistic:  2.19 on 1 and 7 DF,  p-value: 0.1825
lm.HP.f <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP.f) #

##
## Call:
## lm(formula = relinincrease ~ C.fixed3, data = growth[growth$Prey ==
##      "HP" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.86859 -0.12767 -0.00792  0.28699  0.74476
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.6570     0.4669   3.549  0.00935 **
## C.fixed3       0.9753     0.2953   3.303  0.01307 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4839 on 7 degrees of freedom
## Multiple R-squared:  0.6091, Adjusted R-squared:  0.5533
## F-statistic: 10.91 on 1 and 7 DF,  p-value: 0.01307
lm.HP.n <- lm(relincrease~C.fixed3,data=growth[growth$Prey=='HP'&growth$Fed=='N',]); summary(lm.HP.n) #

##
## Call:
## lm(formula = relinincrease ~ C.fixed3, data = growth[growth$Prey ==
##      "HP" & growth$Fed == "N", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.225199 -0.113317  0.005071  0.097854  0.232258
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.1518     0.1637   7.035 0.000205 ***
## C.fixed3       0.4092     0.1953   2.095 0.074397 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1625 on 7 degrees of freedom
## Multiple R-squared:  0.3854, Adjusted R-squared:  0.2976
## F-statistic:  4.39 on 1 and 7 DF,  p-value: 0.0744
plot(growth$C.fixed2/1000,growth$relincrease,pch=c(21,22)[growth$Fed],bg=preycolvec[growth$Prey],las=1,

## Warning in arrows(C.summ[, 5]/1000, I.summ[, 5] + I.summ$se, C.summ[, 5]/
## 1000, : zero-length arrow is of indeterminate angle and so skipped

```

```
TukeyHSD(aov(C.fixed3~Fed*as.factor(Light),data=growth[growth$Prey=='SM',]))
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = C.fixed3 ~ Fed * as.factor(Light), data = growth[growth$Prey == "SM", ])
##
## $Fed
##      diff      lwr      upr p adj
## Y-N 3.283452 2.715732 3.851172    0
##
## $`as.factor(Light)`
##      diff      lwr      upr      p adj
## 50-10 2.6885524 1.8371724 3.539932 0.0000061
## 100-10 3.6647889 2.8134090 4.516169 0.0000002
## 100-50 0.9762366 0.1248566 1.827616 0.0249375
##
## $`Fed:as.factor(Light)`
##      diff      lwr      upr      p adj
## Y:10-N:10 1.4414436 -0.07447034 2.957358 0.0658299
## N:50-N:10 1.1936589 -0.32225503 2.709573 0.1592640
## Y:50-N:10 5.6248894 4.10897548 7.140803 0.0000004
## N:100-N:10 2.3966702 0.88075630 3.912584 0.0019704
## Y:100-N:10 6.3743512 4.85843726 7.890265 0.0000001
## N:50-Y:10 -0.2477847 -1.76369864 1.268129 0.9926408
## Y:50-Y:10 4.1834458 2.66753187 5.699360 0.0000094
## N:100-Y:10 0.9552266 -0.56068730 2.471141 0.3407546
## Y:100-Y:10 4.9329076 3.41699365 6.448822 0.0000016
## Y:50-N:50 4.4312305 2.91531656 5.947144 0.0000051
## N:100-N:50 1.2030113 -0.31290261 2.718925 0.1542413
## Y:100-N:50 5.1806923 3.66477834 6.696606 0.0000009
## N:100-Y:50 -3.2282192 -4.74413312 -1.712305 0.0001313
## Y:100-Y:50 0.7494618 -0.76645216 2.265376 0.5786171
## Y:100-N:100 3.9776810 2.46176701 5.493595 0.0000160
```

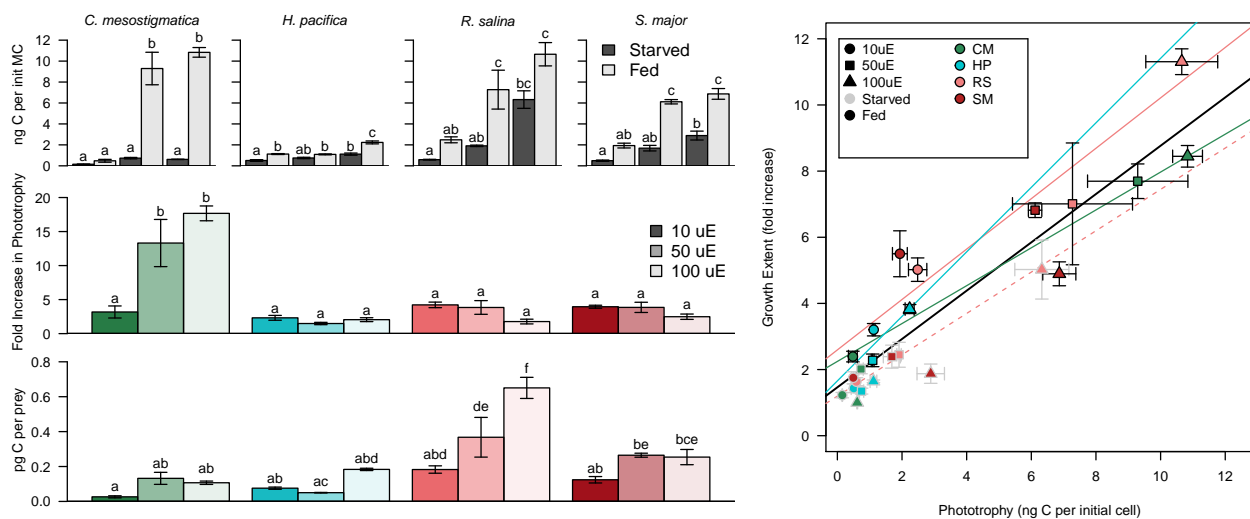




Figure 6, Revision: Photosynthetic contributions to growth

```

layout(matrix(c(8,1,2,3,4,rep(7,3),9,5,5,5,5,rep(7,3),10,6,6,6,6,rep(7,3)),nrow=3,ncol=8,byrow=TRUE));

growth$C.fixed3 <- growth$C.fixed2/1000 # convert from pg to ng
growth$C.per.prey <- growth$C.fixed2/growth$TotPreyCons
growth$C.fixed.perMC.C <- growth$C.fixed3/growth$MC.C # convert from per MC cell to per MC ng C

xcoords <- c(1.2,3.4,5.6)
xcoords2 <- c(.7,1.7,2.9,3.9,5.1,6.1)
#quartz(height=3.5,width=7.5)
par(mar=c(1,1,0.5,0.5))
#layout(matrix(c(7,1,1,1,2,2,3,3,3,4,4,4,rep(6,6),8,rep(5,3*4),rep(6,6)),nrow=2,ncol=19,byrow=TRUE))

# Row 1: Photosynthate
ymax <- 50*12.01/44.01; ymin <- 0; bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='CM',])

bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='HP',],las=1,legend=FALSE,leg.lab=c('Starv'))
bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='RS',],las=1,legend=FALSE,ylim=c(ymin,ymax))
bargraph.CI(Light,C.fixed3,group=Fed,data=growth[growth$Prey=='SM',],las=1,legend=TRUE,leg.lab=c('Starv'))

# Second row: fold difference
xcoords <- c(1,2,3,4.5,5.5,6.5,8,9,10,11.5,12.5,13.5)

bargraph.CI(Prey,C.fixed2/abs(deltaCfixed-C.fixed2),group=Light,data=growth[growth$Fed=='Y',],legend=FALSE)
#TukeyHSD(aov(C.fixed2/abs(deltaCfixed-C.fixed2)~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# Third row: Carbon fixed per prey ingested
bargraph.CI(Prey,C.per.prey,group=Light,data=growth[growth$Fed=='Y',],legend=FALSE,err.width=0.05,las=3)
#TukeyHSD(aov(C.per.prey~as.factor(Light)*Prey,data=growth[growth$Fed=='Y',]))

# FOURTH PLOT: total photosynthate vs growth extent
par(mar=c(4,5,.5,0.5))

lm.all <- lm(growth$relincrease~growth$C.fixed.perMC.C); summary(lm.all) #signif.; F-stat = 310.2, p-val

##
## Call:
## lm(formula = growth$relincrease ~ growth$C.fixed.perMC.C)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6053 -0.7915 -0.0842  0.5028  3.4804
##
## Coefficients:

```

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.47104    0.19640    7.49 1.58e-10 ***
## growth$C.fixed.perMC.C 0.52880    0.03003   17.61 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.214 on 70 degrees of freedom
## Multiple R-squared:  0.8159, Adjusted R-squared:  0.8132
## F-statistic: 310.2 on 1 and 70 DF,  p-value: < 2.2e-16
lm.RS.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='RS'&growth$Fed=='Y',]); summary(lm.f)

##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
## "RS" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7067 -0.5820 -0.3065  0.5846  2.8392
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.29289    0.88856    3.706 0.007596 **
## C.fixed.perMC.C  0.41956    0.07056    5.946 0.000572 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.408 on 7 degrees of freedom
## Multiple R-squared:  0.8347, Adjusted R-squared:  0.8111
## F-statistic: 35.36 on 1 and 7 DF,  p-value: 0.0005724
lm.RS.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='RS'&growth$Fed=='N',]); summary(lm.f)

##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
## "RS" & growth$Fed == "N", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0589 -0.4481 -0.1226  0.1940  1.5581
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.27520    0.44228    2.883 0.02354 *
## C.fixed.perMC.C  0.39691    0.07654    5.185 0.00127 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8509 on 7 degrees of freedom
## Multiple R-squared:  0.7934, Adjusted R-squared:  0.7639
## F-statistic: 26.89 on 1 and 7 DF,  p-value: 0.001273
lm.SM.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='SM'&growth$Fed=='Y',]); summary(lm.f)

```

```
##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##      "SM" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.45815 -1.12985  0.05021  1.03924  1.31004
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.40066    0.90738   5.952 0.000569 ***
## C.fixed.perMC.C  0.04773    0.11603   0.411 0.693081
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.168 on 7 degrees of freedom
## Multiple R-squared:  0.02361,    Adjusted R-squared:  -0.1159
## F-statistic: 0.1693 on 1 and 7 DF,  p-value: 0.6931
lm.SM.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='SM'&growth$Fed=='N',]); summary(lm.SM.n)

##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##      "SM" & growth$Fed == "N", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.64964 -0.41897 -0.05582  0.23975  0.89258
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.77948    0.34584   5.145 0.00133 **
## C.fixed.perMC.C  0.09641    0.12672   0.761 0.47162
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5295 on 7 degrees of freedom
## Multiple R-squared:  0.07637,    Adjusted R-squared:  -0.05557
## F-statistic: 0.5788 on 1 and 7 DF,  p-value: 0.4716
lm.CM.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='CM'&growth$Fed=='Y',]); summary(lm.CM.f)

##
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##      "CM" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.76078 -0.38033 -0.08572  0.36568  0.64725
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```

## (Intercept)      2.3300      0.2963      7.863 0.000102 ***
## C.fixed.perMC.C   0.5557      0.0350     15.877 9.54e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5114 on 7 degrees of freedom
## Multiple R-squared:  0.973, Adjusted R-squared:  0.9691
## F-statistic: 252.1 on 1 and 7 DF, p-value: 9.538e-07
lm.CM.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='CM'&growth$Fed=='N',]); summary(lm.CM.n)

##
## Call:
## lm(formula = relinincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
## "CM" & growth$Fed == "N", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.5195 -0.4890  0.1743  0.2045  0.6383
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.9986      0.3304   3.022  0.0193 *
## C.fixed.perMC.C   0.8283      0.5854   1.415  0.2000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4553 on 7 degrees of freedom
## Multiple R-squared:  0.2224, Adjusted R-squared:  0.1113
## F-statistic: 2.002 on 1 and 7 DF, p-value: 0.2
lm.HP.f <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='HP'&growth$Fed=='Y',]); summary(lm.HP.f)

##
## Call:
## lm(formula = relinincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
## "HP" & growth$Fed == "Y", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.13493 -0.16503  0.01446  0.30774  0.76814
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.0048      0.4981   4.025  0.00503 **
## C.fixed.perMC.C   0.4338      0.1815   2.390  0.04816 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5743 on 7 degrees of freedom
## Multiple R-squared:  0.4494, Adjusted R-squared:  0.3707
## F-statistic: 5.713 on 1 and 7 DF, p-value: 0.04816
lm.HP.n <- lm(relincrease~C.fixed.perMC.C,data=growth[growth$Prey=='HP'&growth$Fed=='N',]); summary(lm.HP.n)

##

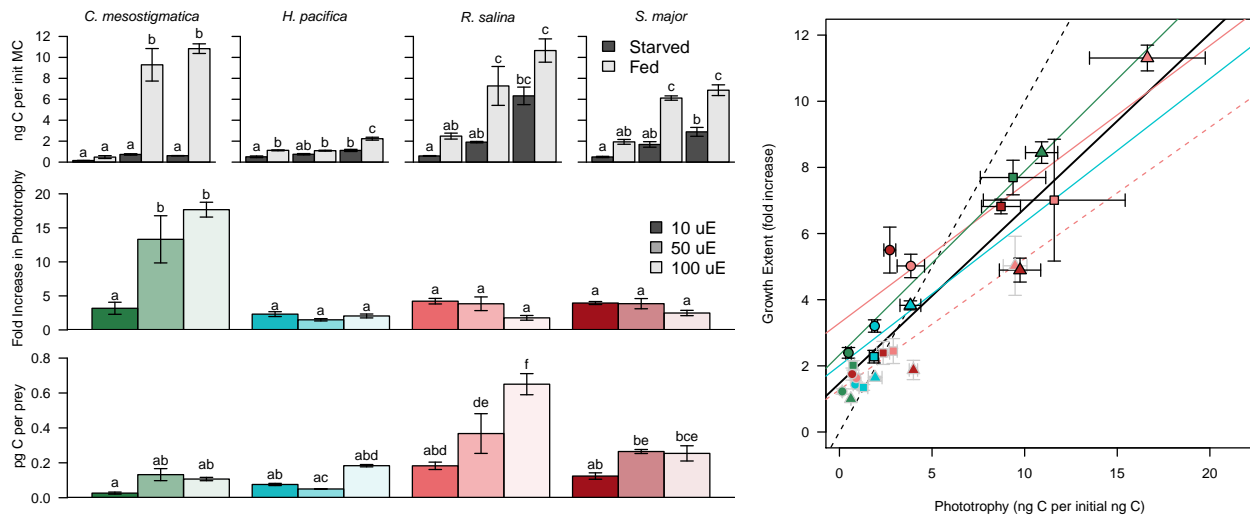
```

```
## Call:
## lm(formula = relincrease ~ C.fixed.perMC.C, data = growth[growth$Prey ==
##      "HP" & growth$Fed == "N", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.2453 -0.1470  0.0246  0.1520  0.1974
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.2910      0.1594   8.100 8.42e-05 ***
## C.fixed.perMC.C    0.1358      0.1080   1.258   0.249
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1872 on 7 degrees of freedom
## Multiple R-squared:  0.1844, Adjusted R-squared:  0.06786
## F-statistic: 1.582 on 1 and 7 DF,  p-value: 0.2488
plot(growth$C.fixed.perMC.C, growth$relincrease, pch=c(21,22)[growth$Fed], bg=preycolvec[growth$Prey], las=1)

## Warning in arrows(C.summ[, 5], I.summ[, 5] + I.summ$se, C.summ[, 5],
## I.summ[, 5] : zero-length arrow is of indeterminate angle and so skipped
TukeyHSD(aov(C.fixed3~Fed*as.factor(Light), data=growth[growth$Prey=='SM',]))

##      Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = C.fixed3 ~ Fed * as.factor(Light), data = growth[growth$Prey == "SM", ])
##
## $Fed
##      diff      lwr      upr p adj
## Y-N 3.283452 2.715732 3.851172    0
##
## $`as.factor(Light)`
##      diff      lwr      upr    p adj
## 50-10  2.6885524 1.8371724 3.539932 0.0000061
## 100-10 3.6647889 2.8134090 4.516169 0.0000002
## 100-50 0.9762366 0.1248566 1.827616 0.0249375
##
## $`Fed:as.factor(Light)`
##      diff      lwr      upr    p adj
## Y:10-N:10  1.4414436 -0.07447034 2.957358 0.0658299
## N:50-N:10  1.1936589 -0.32225503 2.709573 0.1592640
## Y:50-N:10  5.6248894 4.10897548 7.140803 0.0000004
## N:100-N:10 2.3966702 0.88075630 3.912584 0.0019704
## Y:100-N:10 6.3743512 4.85843726 7.890265 0.0000001
## N:50-Y:10 -0.2477847 -1.76369864 1.268129 0.9926408
## Y:50-Y:10  4.1834458 2.66753187 5.699360 0.0000094
## N:100-Y:10 0.9552266 -0.56068730 2.471141 0.3407546
## Y:100-Y:10 4.9329076 3.41699365 6.448822 0.0000016
## Y:50-N:50  4.4312305 2.91531656 5.947144 0.0000051
## N:100-N:50 1.2030113 -0.31290261 2.718925 0.1542413
## Y:100-N:50 5.1806923 3.66477834 6.696606 0.0000009
```

```
## N:100-Y:50 -3.2282192 -4.74413312 -1.712305 0.0001313
## Y:100-Y:50 0.7494618 -0.76645216 2.265376 0.5786171
## Y:100-N:100 3.9776810 2.46176701 5.493595 0.0000160
```



## Supplementary Figures, Revision: Timeseries of cells and pigments

```
# Choose the data columns to use, their names, and their maxima
#datcols <- c(8,9,30,dim(dat)[2]-2,dim(dat)[2]-1)
datcols <- c(which(names(dat)=='MC_cellspmL'),which(names(dat)=='Prey_cellspmL'),which(names(dat)=='Plas
ylabstrs <- c('MC (cells/mL)','Prey (cells/mL)','Plastids (per MC cell)','MC chl (pg/cell)','MC chl (pg
ymax <- c(10000,25000,30,55,85,100)

# We will partition data by light level
lightvec <- c(10,50,100)
titlestr <- paste(as.character(lightvec),'uE'); titlestr <- rbind(titlestr,c(rep('',3)),c(rep('',3)),c(

# Iterate over different prey types
preyvec <- c('CM','HP','RS','SM')
preycolvec <- c(CMcol,HPcol,RScol,SMcol)

# Step 1: choose your prey type & subset data
for(k in 1:length(preyvec)){

# Step 1: Choose the prey and subset data accordingly
preychoice <- preyvec[k]
dat.hold2 <- dat[dat$Prey==preychoice,]

par(mar=c(1,4,1,0.1),mfcol=c(length(datcols),length(lightvec)))
# Note that we've used the argument "mfcol" instead of "mfrow." This ensures that the subsequent mega-p

for(j in 1:length(lightvec)){

# Step 2: Subset the data again for appropriate light level
dat.hold <- dat.hold2[dat.hold2$Light==lightvec[j],]
```

```

# Step 3: Create summary stats.
summ.MC<-summarySE(data=dat.hold,measurevar="MC_cellspmL",groupvars=c("ExptDay", 'Fed'),na.rm=TRUE)
summ.prey<-summarySE(data=dat.hold,measurevar="Prey_cellspmL",groupvars=c("ExptDay", 'Fed'),na.rm=TRUE)
summ.chl<-summarySE(data=dat.hold,measurevar="chl_p_cell",groupvars=c("ExptDay", 'Fed'),na.rm=TRUE)
summ.chl.p.mL <- summarySE(data=dat.hold,measurevar='chl_p_mL',groupvars=c("ExptDay", 'Fed'),na.rm=TRUE)
summ.chl.p.C <- summarySE(data=dat.hold,measurevar='ChlperC',groupvars=c("ExptDay", 'Fed'),na.rm=TRUE)
summ.Plastids<-summarySE(data=dat.hold,measurevar="PlastidCount",groupvars=c("ExptDay", 'Fed'),na.rm=TRUE)

# Step 4: Make all the plots
for(i in 1:length(datcols)){

# Create axes using raw data
plot(dat.hold$ExptDay, dat.hold[,datcols[i]], type='n', las=1, xlab='', main=titlestr[i,j],ylim=c(0,ymax))

if(i == 1){ summ.use <- summ.MC }; if(i == 2){ summ.use <- summ.prey }; if(i == 4){ summ.use <- summ.chl.p.mL }; if(i == 5){ summ.use <- summ.Plastids }

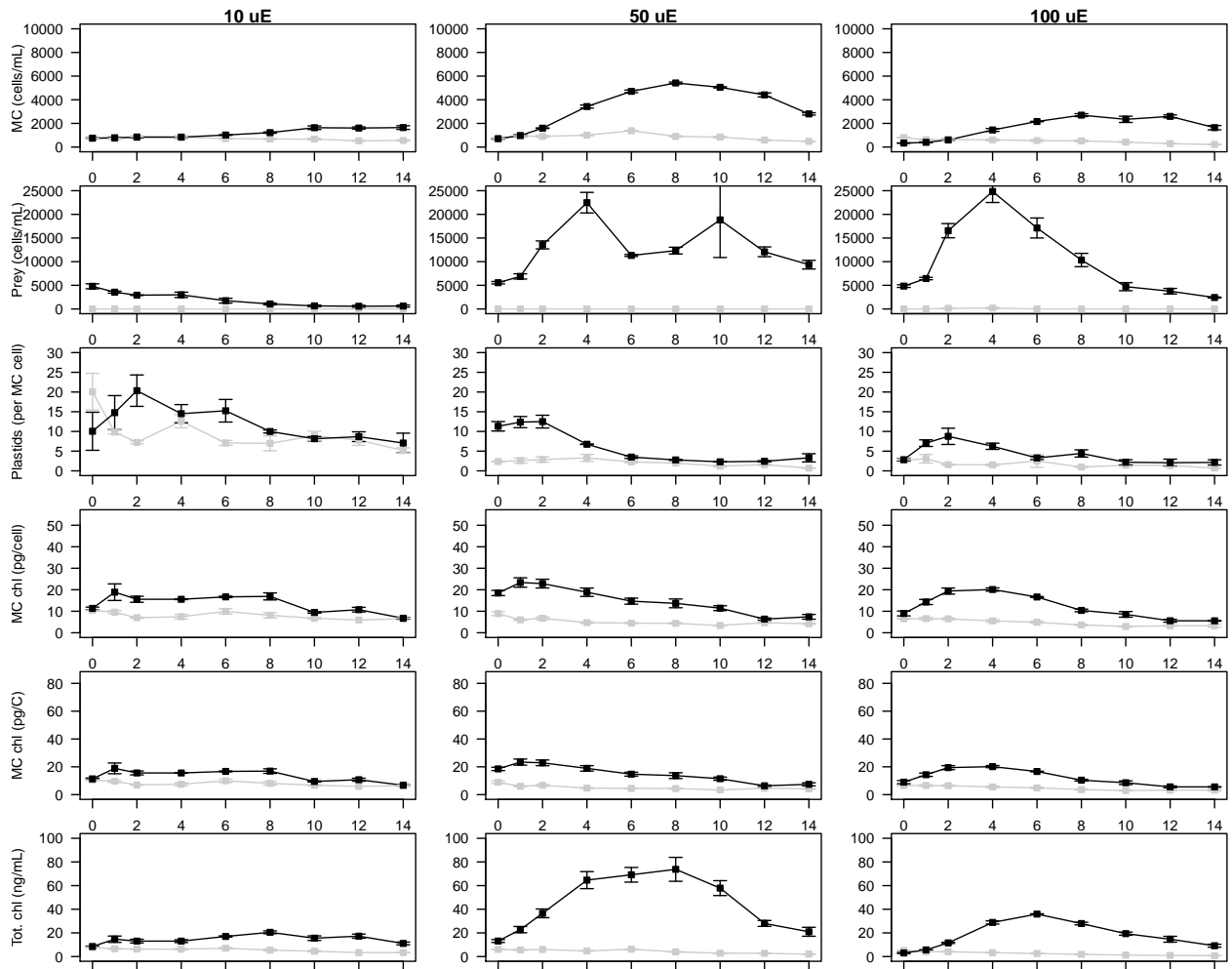
# Plot lines connecting means
lines(summ.use[summ.use$Fed=='N'],$ExptDay,summ.use[summ.use$Fed=='N'],[,4],col= Starvedcol); lines(summ.use[summ.use$Fed=='Y'],$ExptDay,summ.use[summ.use$Fed=='Y'],[,4],col= Fedcol)

# Plot std error
summ.use.Y <- summ.use[summ.use$Fed=="Y",]; summ.use.N <- summ.use[summ.use$Fed=="N",]
arrows(summ.use.Y$ExptDay,summ.use.Y[,4]+summ.use.Y$se,summ.use.Y$ExptDay,summ.use.Y[,4]-summ.use.Y$se,angle=90)

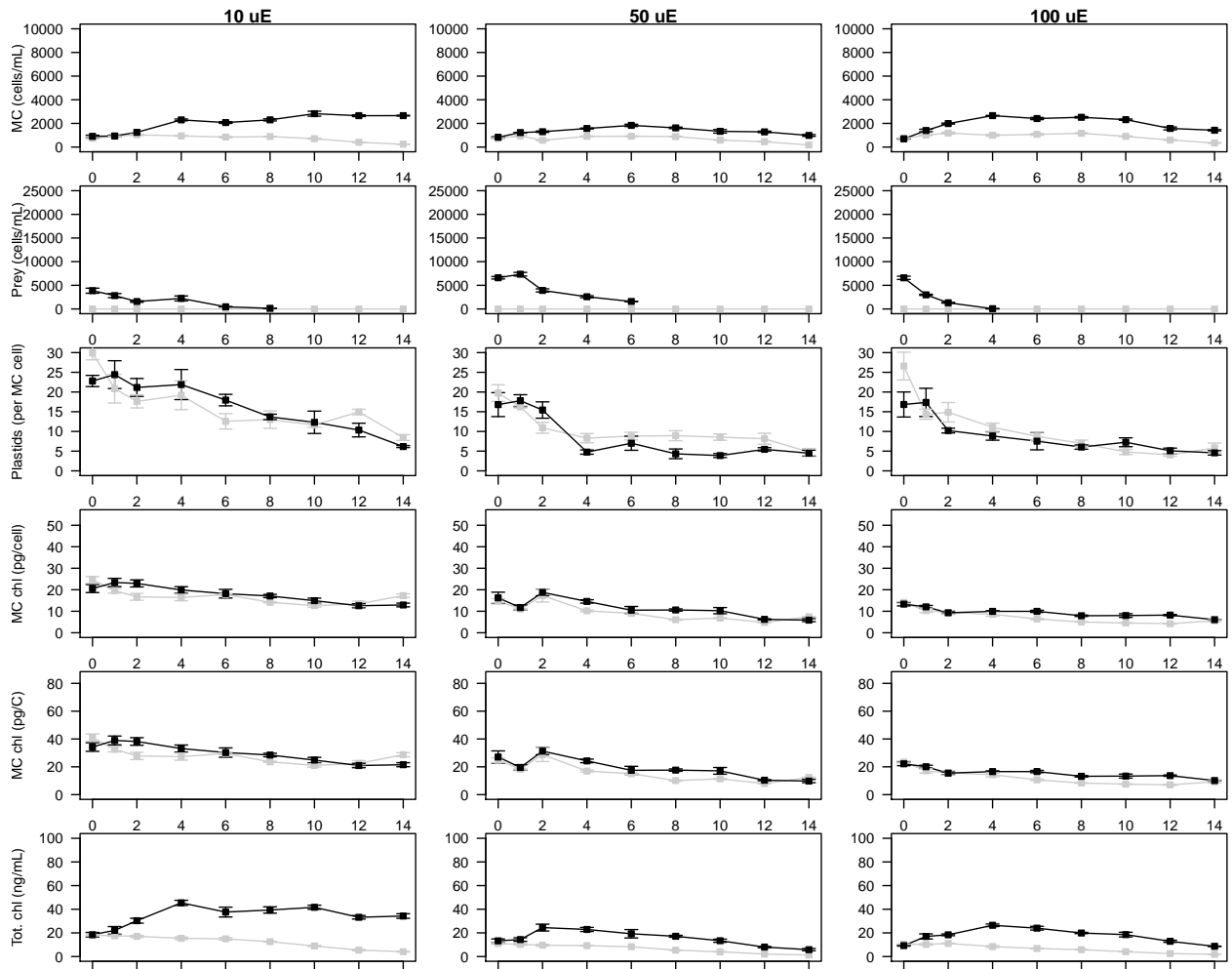
# Plot means
points(summ.use$ExptDay,summ.use[,4],pch=22,col=c(Starvedcol,Fedcol)[summ.use$Fed],bg=c(Starvedcol,Fedcol)[summ.use$Fed])

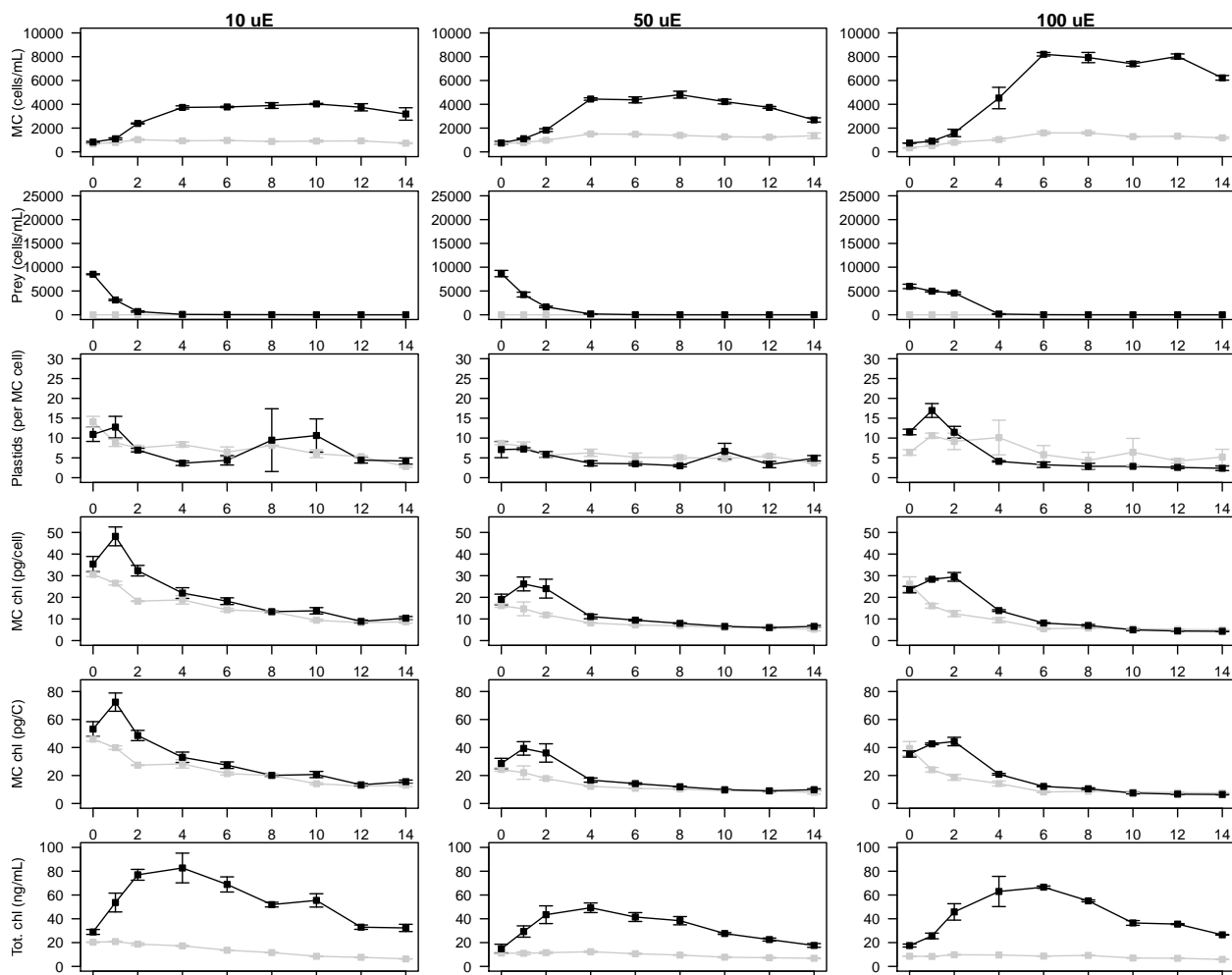
}}
}

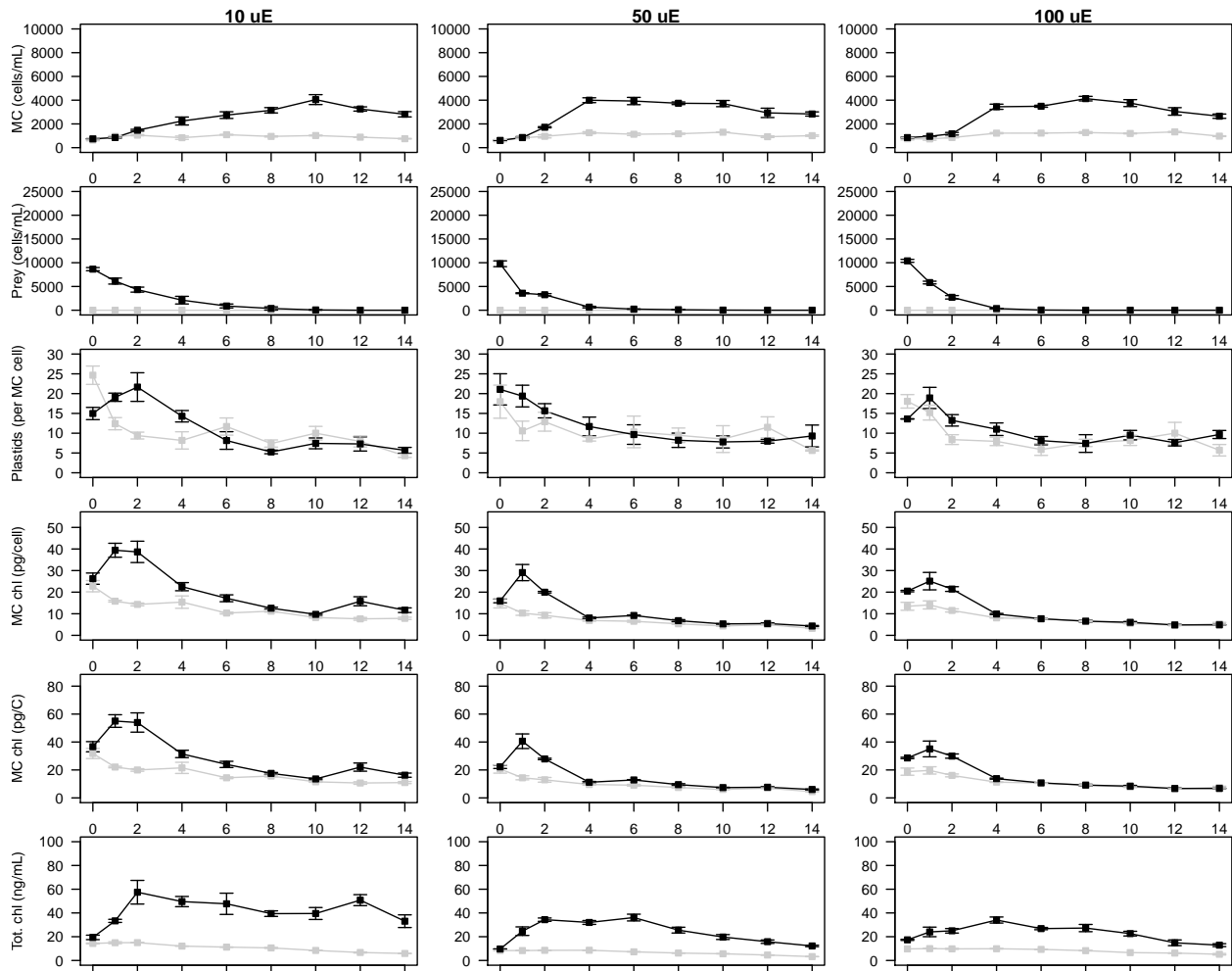
```











Supplementary Figures: Photophysiology timeseries

```
# Choose the data columns to use, their names, and their maxima
datcols <- c(12,21,dim(dat)[2]-4,dim(dat)[2]-3) # data columns to use. CHECK THIS CAREFULLY
ylabstrs <- c('Photosynth. Eff. (Fv/Fm)', 'ETR', 'PI_chl', 'PI_cell') # y-labels
ymax <- rbind(rep(0.6,3),c(20,80,150),c(2,5,10),c(30,100,150))
ymin <- c(0.1,0,0,0)

# We will partition data by light level
lightvec <- c(10,50,100)
titlestr <- paste(as.character(lightvec),'uE'); titlestr <- rbind(titlestr,c(rep('',4)),c(rep('',4)),c(

# Iterate over different prey types
preyvec <- c('CM','HP','RS','SM')

# Step 1: choose your prey type & subset data

for(k in 1:length(preyvec)){

# Step 1: Choose the prey and subset data accordingly
preychoice <- preyvec[k]
```

```

dat.hold2 <- dat[dat$Prey==preychoice,]
crypto.hold2 <- crypto.dat[crypto.dat$Prey==preychoice,]

par(mar=c(2,4,2,1),mfcol=c(length(datcols),length(lightvec)))
# Note that we've used the argument "mfcol" instead of "mfrow." This ensures that the subsequent mega-p

for(j in 1:length(lightvec)){

  # Step 2: Subset the data again for appropriate light level
  dat.hold <- dat.hold2[dat.hold2$Light==lightvec[j],]
  crypto.hold <-crypto.hold2[crypto.hold2$Light==lightvec[j],]
  # Step 3: Create summary stats.
  summ.FvFm<-summarySE(data=dat.hold,measurevar="FvFm",groupvars=c("ExptDay","Fed"),na.rm=TRUE); crypto.F
  summ.ETR <- summarySE(data=dat.hold,measurevar="ETR_I",groupvars=c("ExptDay","Fed"),na.rm=TRUE); crypto

  summ.PIch1<-summarySE(data=dat.hold,measurevar="PI_ch1",groupvars=c("ExptDay","Fed"),na.rm=TRUE); crypto
  summ.PIch1<-summarySE(data=dat.hold,measurevar="PI_cell",groupvars=c("ExptDay","Fed"),na.rm=TRUE); cryp

  # Step 4: Make all the plots
  for(i in 1:length(datcols)){

    # Create axes using raw data
    plot(dat.hold$ExptDay, dat.hold[,datcols[i]], type='n', las=1, ylab=ylabstrs[i], xlab='', main=titlestr

    if(i == 1){ summ.use <- summ.FvFm; crypto.use<-crypto.FvFm }; if(i == 2){ summ.use <- summ.ETR; crypto.

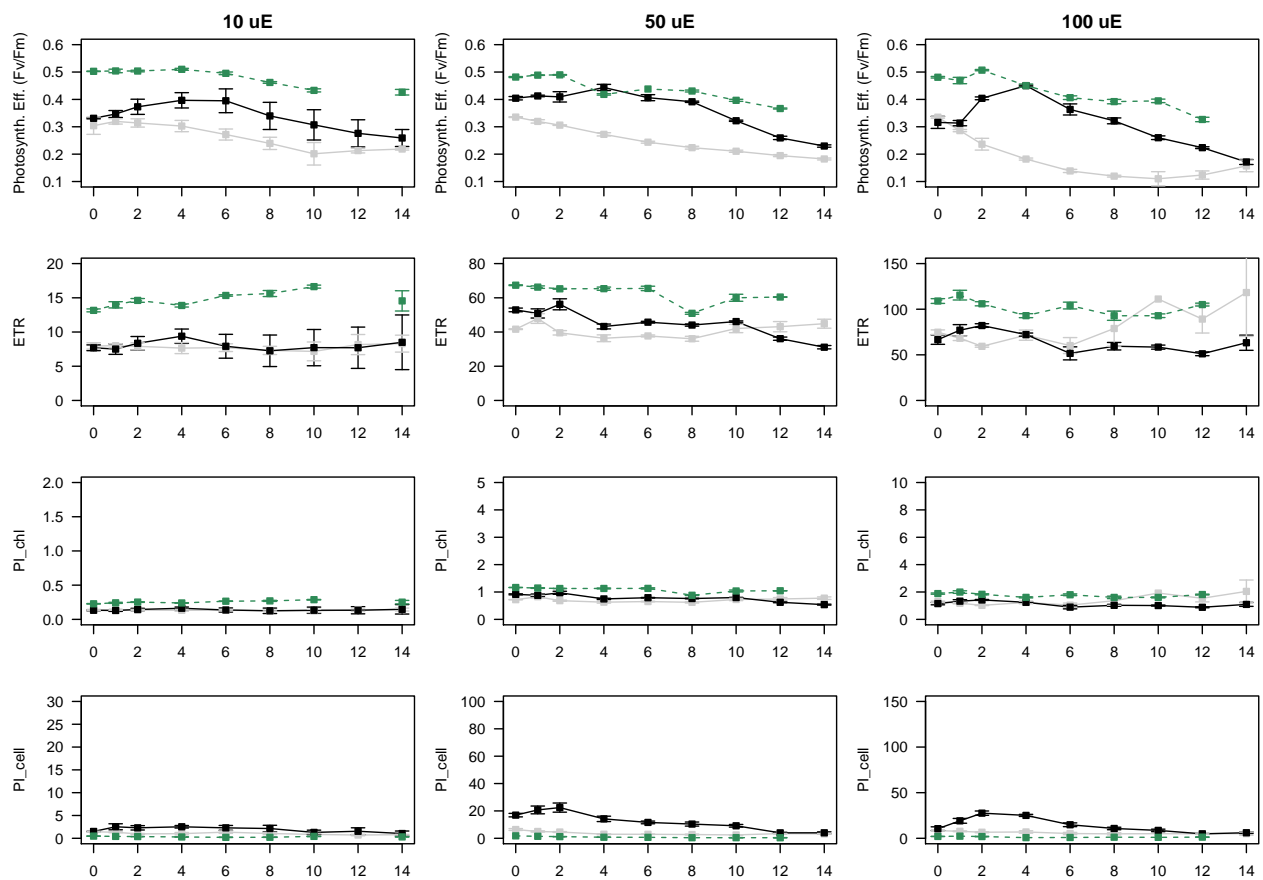
    # Plot lines connecting means
    lines(summ.use[summ.use$Fed=='N'],)$ExptDay,summ.use[summ.use$Fed=='N'],[,4],col= Starvedcol); lines(summ

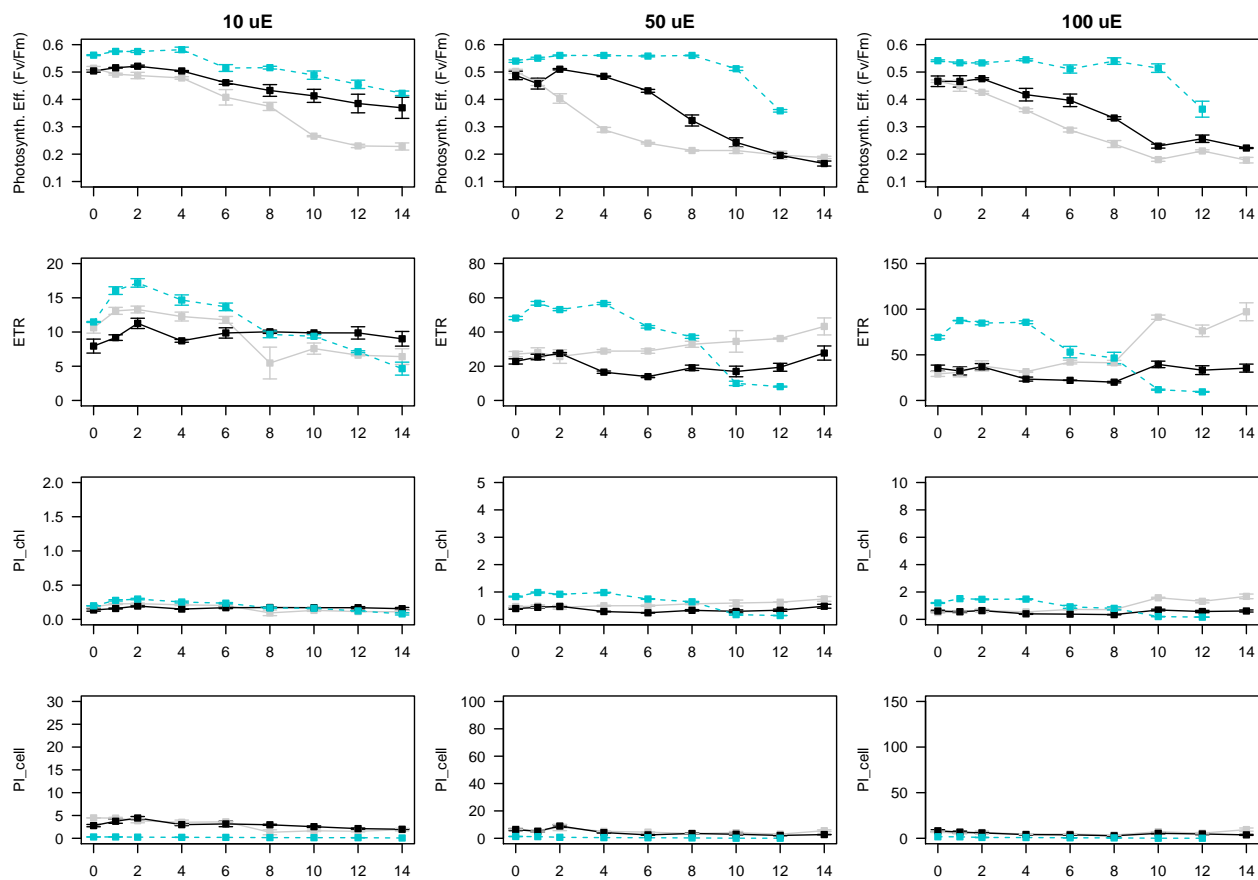
    # Plot std error
    summ.use.Y <- summ.use[summ.use$Fed=="Y",]; summ.use.N <- summ.use[summ.use$Fed=="N",]
    arrows(summ.use.Y$ExptDay,summ.use.Y[,4]+summ.use.Y$se,summ.use.Y$ExptDay,summ.use.Y[,4]-summ.use.Y$se,

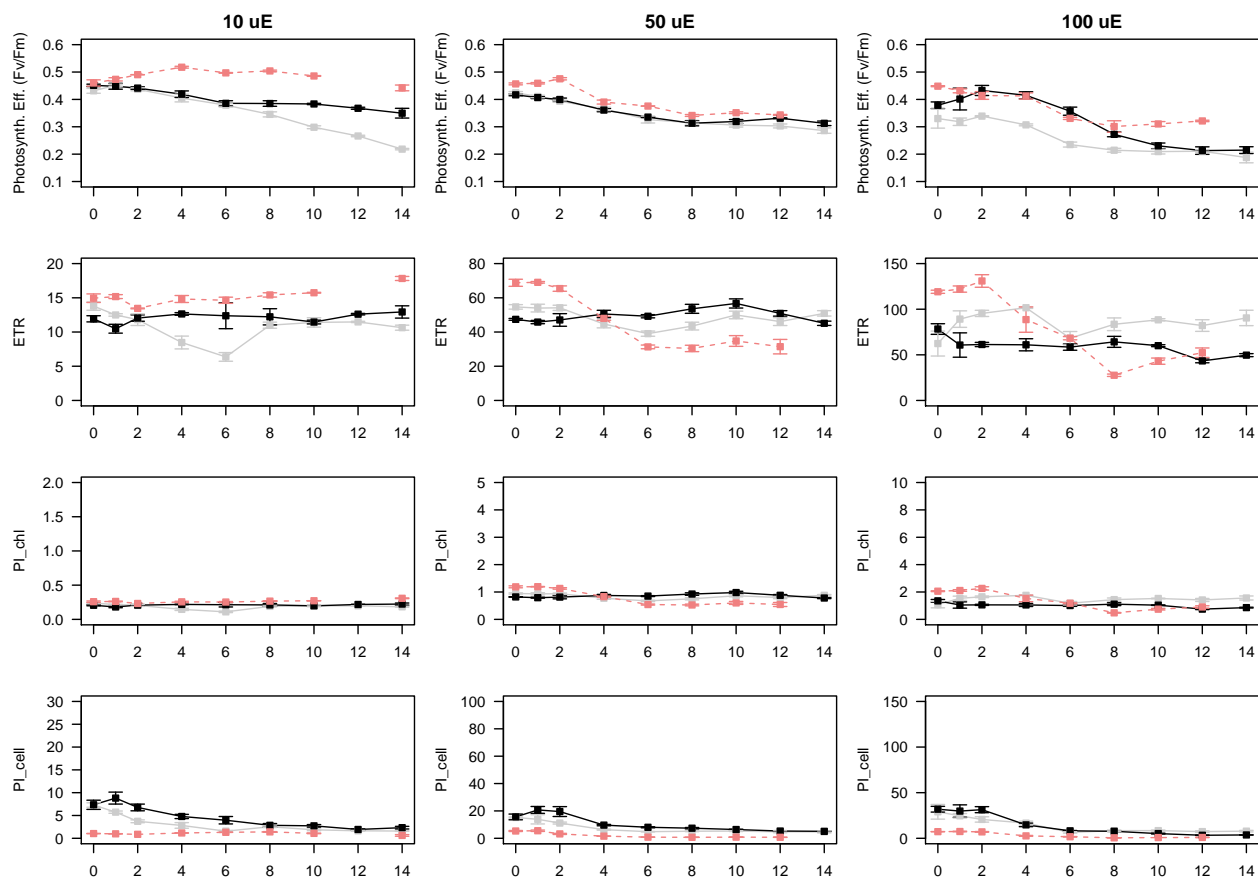
    # Plot means
    points(summ.use$ExptDay,summ.use[,4],pch=22,col=c(Starvedcol,Fedcol)[summ.use$Fed],bg=c(Starvedcol,Fedcol

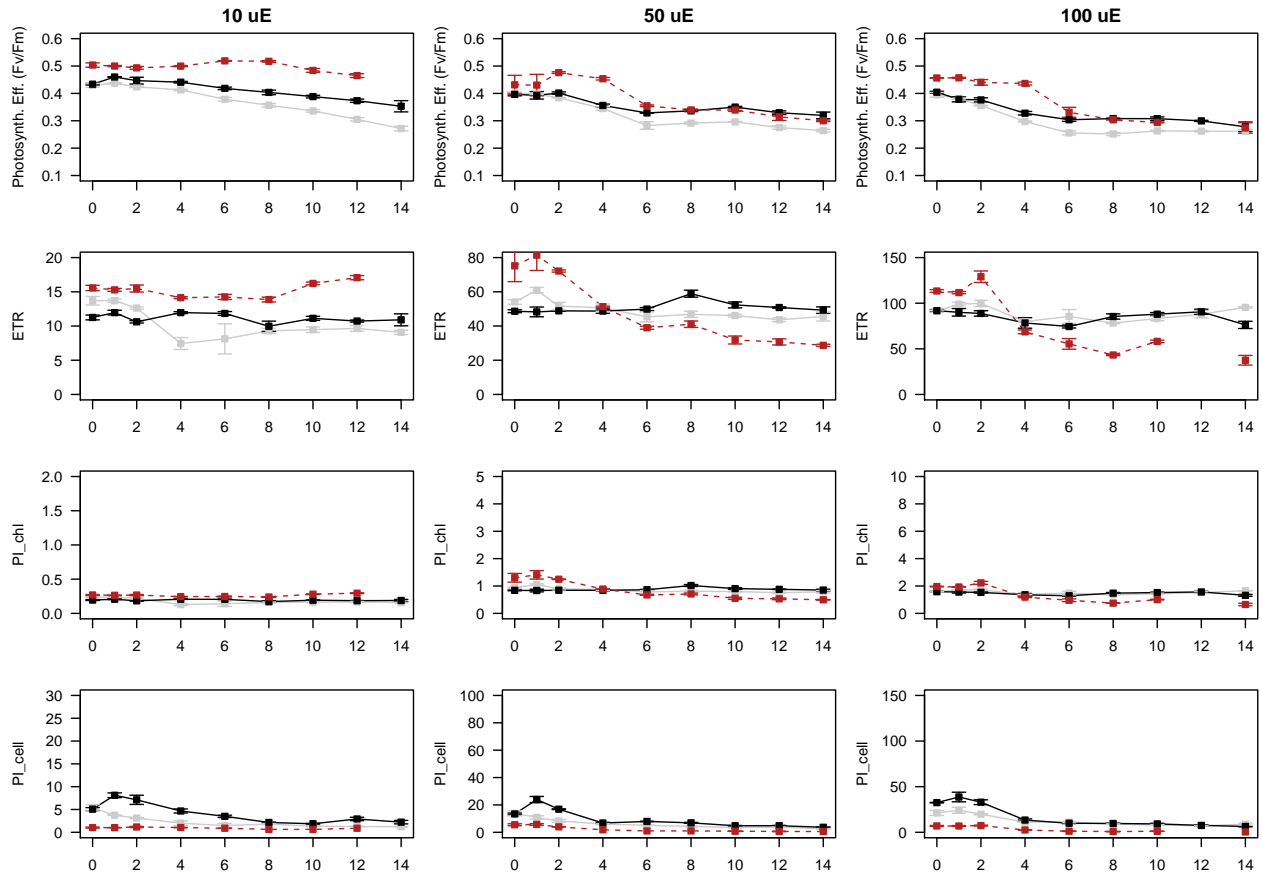
  }}
}

```









Supplementary Figures: Photophysiology timeseries, revision 1

```
# Choose the data columns to use, their names, and their maxima
datcols <- c(which(names(dat)=='FvFm'),which(names(dat)=='a'),which(names(dat)=='Pmax'),which(names(dat)
ylabstrs <- c('Photosynth. Eff. (Fv/Fm)', 'alpha', 'Pmax', 'PI_chl', 'PI_C', 'PI_cell') # y-labels
ymax <- rbind(rep(0.6,3),c(2.3,3,3),c(150,200,250),c(2,5,10)*12.01/44.01,c(100,400,500)*12.01/44.01,c(3
ymin <- c(0.1,0,0,0,0,0)

# We will partition data by light level
lightvec <- c(10,50,100)
titlestr <- paste(as.character(lightvec),'uE'); titlestr <- rbind(titlestr,c(rep('',3)),c(rep('',3)),c(

# Iterate over different prey types
preyvec <- c('CM','HP','RS','SM')

# Step 1: choose your prey type & subset data
for(k in 1:length(preyvec)){

# Step 1: Choose the prey and subset data accordingly
preychoice <- preyvec[k]
dat.hold2 <- dat[dat$Prey==preychoice,]
crypto.hold2 <- crypto.dat[crypto.dat$Prey==preychoice,]
```



```

par(mar=c(1,4,1,.1),mfcol=c(length(datcols),length(lightvec)))
# Note that we've used the argument "mfcol" instead of "mfrow." This ensures that the subsequent mega-p

for(j in 1:length(lightvec)){

# Step 2: Subset the data again for appropriate light level
dat.hold <- dat.hold2[dat.hold2$Light==lightvec[j],]
crypto.hold <-crypto.hold2[crypto.hold2$Light==lightvec[j],]
# Step 3: Create summary stats.
summ.FvFm<-summarySE(data=dat.hold,measurevar="FvFm",groupvars=c("ExptDay", 'Fed'),na.rm=TRUE); crypto.F
summ.ETR <- summarySE(data=dat.hold,measurevar='PI_C',groupvars=c("ExptDay", 'Fed'),na.rm=TRUE); crypto.

summ.alpha <- summarySE(data=dat.hold,measurevar='a',groupvars=c("ExptDay", 'Fed'),na.rm=TRUE); crypto.a
summ.Pmax <- summarySE(data=dat.hold,measurevar='Pmax',groupvars=c("ExptDay", 'Fed'),na.rm=TRUE);
if(preychoice=='CM'){if(j == 3){summ.Pmax[13,4]<-NaN}}
crypto.Pmax <- summarySE(data=crypto.hold,measurevar='Pmax',groupvars=c("ExptDay"),na.rm=TRUE); crypto.

summ.PIch1<-summarySE(data=dat.hold,measurevar="PI_ch1",groupvars=c("ExptDay", 'Fed'),na.rm=TRUE); crypto
summ.PIch1<-summarySE(data=dat.hold,measurevar="PI_cell",groupvars=c("ExptDay", 'Fed'),na.rm=TRUE); cry

# Step 4: Make all the plots
for(i in 1:length(datcols)){

# Create axes using raw data
plot(dat.hold$ExptDay, dat.hold[,datcols[i]], type='n', las=1, xlab='', main=titlestr[i,j],ylim=c(ymin[

if(i == 1){ summ.use <- summ.FvFm; crypto.use<-crypto.FvFm }; if(i == 2){ summ.use <- summ.alpha; crypto

# Plot lines connecting means
lines(summ.use[summ.use$Fed=='N'],]$ExptDay,summ.use[summ.use$Fed=='N'],[,4],col= Starvedcol); lines(sum

# Plot std error
summ.use.Y <- summ.use[summ.use$Fed=="Y",]; summ.use.N <- summ.use[summ.use$Fed=="N",]
arrows(summ.use.Y$ExptDay,summ.use.Y[,4]+summ.use.Y$se,summ.use.Y$ExptDay,summ.use.Y[,4]-summ.use.Y$se,

# Plot means
points(summ.use$ExptDay,summ.use[,4],pch=22,col=c(Starvedcol,Fedcol)[summ.use$Fed],bg=c(Starvedcol,Fedcol

}}
}

```

